ME

STIC-Biotech/ChemLib

11644

From:

Whiteman, Brian

Sent:

Wednesday, January 11, 2006 6:27 PM

To:

STIC-Biotech/ChemLib

Subject:

seq search

10/822873

SEQ ID NO: 10 and 11

- 1) us patents and published us patent applications
- 2) commercial databases

Thanks

Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Date completed:
Online Time:

Type of Search

NA#______ AA#:_____

S/L:____ Oligomer:_____

Encode/Transl:_____

Structure #:_____Text:____

Inventor:_____ Litigation:____

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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Sequence 22, Application US/0903333

Sequence 22, Application US/0903333

GENERAL INFORMATION:
APPLICANT: VL, De Chao
APPLICANT: Schuur, Eric
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF UTILE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCES:
ADDRESSE: MORRISON & FORESTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                     Sequence 2, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 10631, A
Sequence 1440, A
Sequence 1, Appli
Sequence
Sequence
Sequence
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                                 US-09-549-519-36
US-08-920-234-2
US-08-920-234-2
US-09-285-502-4
US-09-030-338-9
US-09-071-385A-4
US-09-949-016-10631
US-09-949-016-10631
US-09-248-796A-14840
US-08-248-796A-14840
US-08-374-834-1
US-08-644-271-1
US-08-644-271-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACTIBLE
OPERATION SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,333
FILING DATE: 02-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/03,333
FILING DATE:
APPLICATION NUMBER: 40,130
REGISTRATION NUMBER: 40,130
REGISTRATION NUMBER: 40,130
REGISTRATION NUMBER: 34802-20007.00
TELECHOMENICATION INFORMATION:
TELERHONE: 650-813-5600
TELERHONE: 650-813-5600
 .09-489-039A-13241
                                                                                                                                                                                                                                                                                  US-10-016-283-1
US-09-134-000C-3820
US-09-328-714A-4
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
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MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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STRANDEDNESS: siz
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STATE: CA
COUNTRY:
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Query Match
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 Sequence 22, Appl
Sequence 23, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 18, Appl
Sequence 5, Appl
Sequence 33, Appl
Sequence 9549, Appl
Sequence 44, Appl
Sequence 42, Appl
Sequence 2, Appli
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Sequence 8267, Ap
Sequence 8, Appli
                                                                                                                           ; Search time 23 Seconds (without alignments) 363.054 Million cell updates/sec
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                                                                                                                                                                                                                                             1 MTGSTIAPTTDYRNTTATGL......NEKIHRLDGLKPCSLLLQYD 101
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/cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RCOMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-033-428-23

US-09-0514-495-21

US-09-0514-495-23

US-09-151-376-11

US-09-151-376-11

US-09-151-376-11

US-09-151-376-11

US-09-161-357-18

US-09-161-357-18

US-09-161-357-18

US-09-161-357-18

US-09-161-357-18

US-09-161-357-18

US-09-161-357-18

US-09-161-357-18

US-09-161-357-18

US-09-161-780-2

US-09-1780-2

US-09-1780-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                             - protein search, using sw model
                                                                                                                               January 18, 2006, 19:44:52
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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551
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Match Length
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Score

Result Š USE

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/09033428

Sequence 23, Application US/09033428

Sequence 23, Application US/09033428

GENERAL INFORMATION:
APPLICANT: Limparski, Henry
APPLICANT: Lamparski, Henry
APPLICANT: Lamparski, Henry
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CTIT: PALO ALTO
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                                                                                           1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                      1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                          0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,428
FILING DATE:
CLASSIFICATION:
Best Local Similarity 100.0%; Pred. No. 6.9e-60; Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELEFAX: (415) 814-0792
TELEX: 706141 MESNFOERS SFO
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 101; Conservative
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US-09-033-556-10 ; Sequence 10, Application US/09033556 ; Patent No. 6432700

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Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
THEREOF
APPLICANT: Henderson, Daniel R.
APPLICANT: Howeld a Chao
TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
TITLE OF INVENTION & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                           COUNTRY: usa

ZIP: 94304-1018

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
SOFTWARE: FastSEQ for Windows
SOFTWARE: PastSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,556
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 40,130
REGISTRATION NUMBER: 40,130
REGISTRATION NUMBER: 34802-20010.00
TELEFONDIS 650-813-5600
TELEFONDIS 650-813-5600
TELEFAX: 706141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acids
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100.0%; Score 551; DB 2;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0;
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09614495
Patent No. 6436394
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/033,428
FILING DATE: CURLOWN-
ATTORNEY AGENT INFORMATION:

NAME: POLIZZI, CATHERINE M.
REGESTRATION NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
TELEPROME: (415) 813-5600
TELERA: (415) 434-6792
TELERA: (416) 434-6792
TELERA: 706141 MRSNFORES SFO
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acide
TYRE: amino acide
TYRE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09151376

Batent No. 6676935

GENERAL INPORMATION:
APPLICANT: Henderson, D.R.
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REPERENCE: 34802500221
CURRENT APPLICATION NUMBER: US/09/151,376
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 08/669,753
EARLIER FILING DATE: 1996-06-26
EARLIER FILING DATE: 1996-06-26
EARLIER FILING DATE: 1995-06-27
NUMBER: OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO II
LENGTH: 101

LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-09-814-351-18
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US-09-151-376-11
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Sequence 23, Application US/0989883
Patent No. 6585968
GENERAL INFORMATION:
APPLICANT: Little, Andrew
Lamparski, Henry
Schuur, Bric
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTGSTIAPTIDYRNTTATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,883
                                      COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
OPERATING SYSTEM: Windows
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/614,495
FILING DATE: 11-Jul-2000
CLASSIFTCATION: cubrnown>
PRIOR APPLICATION: cubrnown>
PRIOR APPLICATION: cubrnown>
PRIOR APPLICATION: cubrnown>
APPLICATION NUMBER: 09/033,333
FILING DATE: Cubrnown>
MAME: Catherine, Polizzi M
REGERSTATION: NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20007.00
TELEFRONE SO-494-0792
TELEFRONE CIBRACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 101 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: WORRISON & FOERSTER
STREET 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 23
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US-09-898-883-23
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61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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Matches 101; Conservative
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US-09-875-228-5
                                                                                                   US-09-814-357-18
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APPLICANT: YU, De-Chao
APPLICANT: Zhang, Hong
APPLICANT: Zhang, Hong
APPLICANT: ALAng, Hong
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 3402201500
CURRENT APPLICATION NUMBER: 06/191,861
PRIOR FILING DATE: 2001-10-12
RIOR APPLICATION NUMBER: 60/191,861
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 46
SSOFTWARE: FRRESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MIGSTIAPITDYRNTTATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                  GENERAL INFORMATION:
APPLICANT: Yu, De-Chao
APPLICANT: Yu, De-Chao
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION:
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
FILE REFERENCE: 34802201700
CURRENT APPLICATION NUMBER: US/09/814,351
CURRENT APPLICATION NUMBER: 60/192,156
PRIOR PELING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTHARE: PastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 551; DB 2; Length 101; 100.0%; Pred. No. 6.9e-60; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 551; DB 2; Length 101; Best Local Similarity 100.0%; Pred. No. 6.9e-60; Matches 101; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Amino acid sequence for ADP US-09-814-351-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Amino acid sequence for ADP
US-09-814-292-4
  Sequence 18, Application US/09814351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09814292
Patent No. 6852528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 101; Conservative
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LENGTH: 101
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GENERAL INFORMATION:
APPLICANT: Yu, D.
APPLICANT: Henderson, D.R.
APPLICANT: Henderson, D.R.
APPLICANT: Henderson, D.R.
APPLICANT: Henderson, D.R.
APPLICANT: Schuur, E.R.
TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
TITLE OF INVENTION: ENHANCER: US/09/875,228
CURRENT APPLICATION NUMBER: US/09/875,228
CURRENT FILING DATE: 1998-08-03
PRIOR FILING DATE: 1998-08-03
PRIOR PELING DATE: 1998-03-02
PRIOR PILING DATE: 1998-03-02
PRIOR PILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIN Ver. 2.0
LENGTH: 101
TYPE: PRI
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Sequence 18 Application US/09814357

Patent No. 6911200

GENERAL INFORMATION:
APPLICANT: Yu, De-Chao
APPLICANT: Yu, De-Chao
TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
TITLE OF INVENTION: HENGOTHERAPY AND RADIATION
TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
TITLE OF INVENTION: WITHOUT TARGET CELL-SPECIFIC ADENOVIRUS,
TITLE OF INVENTION WINBER: US/09/814,357
CURRENT APPLICATION NUMBER: 08/09/814,357
CURRENT FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 18
SEQ ID NO 18

LENGTH: 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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100.0%; Score 551; DB 2;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 551; DB 2; 100.0%; Pred. No. 6.9e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Amino acid sequence for ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09875228
Patent No. 6916918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Sequence 9549, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
APPLICANT: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9549
                                                                                                               4 STIAPTIDYRNTTATGLTS-ALNLPQVHAFVND-----WASL-DMWWFSI---ALMFVC 52
                                                                      24 LNLPQVHAFVNDWASLDMW---WFSIALM-----FVCLIIMWLICCLKRRRARPPIYRP
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13.3%; Score 73.5; DB 2; Length 521;
Best Local Similarity 30.4%; Pred. No. 1.7;
Matches 31; Conservative 16; Mismatches 32; Indels 23
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| Sacquence 44, Application US/09934289A
| Patent No. 685287|
| GENERAL INFORMATION:
| APPLICANT: Busfield, Samantha J.
| TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED CURRENT APPLICATION NUMBER: US/09/934,289A
| CURRENT APPLICATION NUMBER: US 09/342,767 |
| PRIOR FILING DATE: 1999-06-29 |
| PRIOR FILING DATE: 1999-06-29 |
| PRIOR FILING DATE: 1998-09-03 |
| NUMBER OF ENQ IN NOS: 58 |
| SOFTWARE: FASTER OF OF WINDOWS VERSION 3.0 |
| LENGTH: 239 |
| TYPE: PRT
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Best Local Similarity 35.9%; Pred. No. 1.3;
Matches 14; Conservative 10; Mismatches 11; Indels
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19;
Mismatches
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Conservative
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US-09-934-289A-44
                                                                                                                                                                                                                                                                           US-09-489-039A-9549
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APPLICANT: Yu, De Chao
APPLICANT: Yu, De Chao
APPLICANT: Whenderson, Daniel
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
FILE REFERENCE: CELL-0.1, 122.1
FILE REFERENCE: CELL-0.1, 122.1
CURRENT APPLICATION NUMBER: 60/099,791
PRIOR FILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-09-09
RIOR PILING DATE: 1999-09-09
RIOR FILING DATE: 1999-09-09
ROFWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NOS: 8
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Batent No. 6673601

GENERAL INFORMATION:

APPLICANT: TORDO, NOEL

APPLICANT: PERRIN, PIERRE

APPLICANT: PACOB, YVES

TITLE OF INVENTION: CHIMERIC LYSSAVIRUS NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 03495-0188-00000

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/129,501

PRIOR FILING DATE: 1999-04-15

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 40

LENGTH: 52

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                                 1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDWWWFSIALMFVCLIIMWLIC 60
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Pred. No. 1.5;
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                                                                                                                                                                                  61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                     61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 8, Application US/09392822A; Patent No. 6900049
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Best Local Similarity
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US-09-549-519-33
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US-09-392-822A-8
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TYPE: PRT
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12.9%; Score 71; DB 2; Length 277;
Best Local Similarity 35.9%; Pred. No. 1.6;
Matches 14; Conservative 10; Mismatches 11; Indels
RESULT 15
US-09-934-289A-42
; Sequence 42. Application US/09934289A
; Patent No. 6852837
; GENERAL INFORMATION:
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPENIN'S ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MAIOSH-06-07
; FILE REPERENCE: MAIOSH-06-07
; CURRENT APPLICATION NUMBER: US 09/342,767
; PRIOR PILING DATE: 1999-06-29
; PRIOR PILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42

LEAGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-42
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Search completed: January 18, 2006, 19:48:54 Job time : 23 secs

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us-10-822-873-11.rapbm

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                                                                                                  ; Search time 62 Seconds
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680.657 Million cell updates/sec
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Sequence 1
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-09-814-292-4

US-09-814-292-4

US-09-813-23

US-09-151-376-11

US-09-814-351-18

US-09-814-351-18

US-10-045-116-20

US-10-045-116-20

US-10-139-089-11

US-10-139-089-11

US-10-912-22-49

US-10-912-22-110-49

US-10-938-27-8

US-10-934-289A-44

US-10-932-991-42

US-10-932-991-42

US-10-369-300-10

US-10-369-300-10

US-10-369-300-10

US-10-369-300-10

US-10-369-300-10

US-09-934-289A-42

US-10-369-300-10

US-10-369-300-10

US-10-369-300-10

US-09-934-289A-13
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US-10-066-209-2
US-10-369-300-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 4, Application US/09814292
Patent No. US20020120117A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yu, De-Chao
APPLICANT: Abang, Hong
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: HUMAN UNOTHELIAL CELL SPECIFIC UROPLAKIN
TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 34802201550
CURRENT APPLICATION NUMBER: US/09/814,292
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yu, De Chao
APPLICANT: Yu, De Chao
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
FILE REPERBNCE: 348022001200
CURRENT PAPLICATION NUMBER: US/09/392,822
CURRENT FILING DATE: 1999-09-09
EARLIER APPLICATION NUMBER: 60/099,791
EARLIER APPLICATION NUMBER: 60/099,791
SOFTWARE: PSSESSEQ for Windows Version 3.0
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                                            548, App
1550, App
13, Appl
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440, App
59286, App
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59454, A
6, Appl
6, Appl
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Sequence 900, App
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                                       US-10-322-281-548
US-10-322-281-550
US-10-614-853-12
US-10-745-718-2
US-10-932-991-13
US-10-932-991-13
US-10-939-359-2
US-10-939-359-2
US-10-775-204-470
US-10-282-122A-5948
US-10-282-122A-5948
US-10-882-122A-5948
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US-10-437-963-203585
US-10-437-963-203646
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100.0%; Score 551; DB 3;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0;
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; Sequence 9, Application US/09392822;
; Patent No. US20010053352A1
; GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Adenovirus V
US-09-392-822-9
SEQ ID NO 9
LENGTH: 101
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APPLICANT: Schuur, E.R.
APPLICANT: Schuur, E.R.
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: 05/99/875,228
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/127,834
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
PRIOR PRILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PACENTING DATE: 1098-04
SOFTWARE: PACENTING DATE: 1098-04
SOFTWARE: PACENTING DATE: 1098-04
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIGSTIAPITIDYRNTTATGLISALNIPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Score 551; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                 ; OTHER INFORMATION: Amino acid sequence for ADP US-09-814-292-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
PRIOR APPLICATION NUMBER: 60/191,861
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/09875228
; Patent No. US20020136707A1
; GENERAL INFORMATION:
; APPLICANT: Yu, D.
                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 101; Conservative
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ORGANISM: Adenovirus
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US-09-875-228-5
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Sequence 23, Application US/09898883; Patent No. US20020164799A1 GENERAL INFORMATION: APPLICANT: Little, Andrew Schuur, Eric

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Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MIGSTIAPITIDYRNITATGLISALNIPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,883
FILING DATE: 02-Jul-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CLKRRRARPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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APPLICANT: Schuux, E.R.
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REFERENCE: 34802200021
CURRENT APPLICATION NUMBER: US/09/151,376
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 08/669,753
EARLIER APPLICATION NUMBER: 08/669,753
EARLIER APPLICATION NUMBER: 08/495,034
EARLIER FILING DATE: 1995-06-27
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 11
TYPE: PRT
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <UNKNOWN>
ATTONNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40, 130
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELECOWNUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 23: US-09-898-883-23
                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-151-376-11
; Sequence 11, Application US/09151376
; Publication No. US20030044383A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 101 amino acids
                                                                                    NUMBER OF SEQUENCES: 23
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Gaps

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Indels

Length 101;

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1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWPSIALMFVCLIIMWLIC 60
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                                                                                                                                                                                                                                                                                                                                                                             61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                         100.0%; Score 551; DB 3;
Similarity 100.0%; Pred. No. 8.2e-56;
01; Conservative 0; Mismatches 0;
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence for ADP
US-09-814-351-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 101 amino acids
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Best Local Similarity 100.0<sup>3</sup>
Matches 101; Conservative
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Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yu, De-Chao
APPLICANT: Chen, Yu
APPLICANT: WITH COMBINATION TANGET CELL-SPECIFIC ADENOVIRUS,
TITLE OF INVENTION: WITH COMBINATION TANGET CELL-SPECIFIC ADENOVIRUS,
FILE REFERENCE: 34802201060
CURRENT APPLICATION NUMBER: US/09/814,357
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/192,015
PRIOR APPLICATION NUMBER: 60/192,015
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PARESED FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yu, De-Chao
APPLICANT: Yu, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Henderson, Daniel R.
ATTLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME BNTRY SITE
TILE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME BNTRY SITE
TILE REFERENCE: 348022001700
CURRENT APPLICATION NUMBER: 60/192,156
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FRAEUSEQ for Windows Version 4.0
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                                                                             Length 101;
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                                                                                                                                                                                                                                                                           CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                          100.0%; Score 551; DB 3;
100.0%; Pred. No. 8.2e-56;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Amino acid sequence for ADP US-09-814-357-18
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-814-357-18
, Sequence 18, Application US/09814357
; Publication No. US20030068307A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09814351
Publication No. US20030148520A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                     Query Match
Best Local Similarity 100.
Matches 101, Conservative
  ; ORGANISM: Homo sapiens
US-09-151-376-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-814-351-18
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LENGTH: 101
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APPLICANT: Lamparski, Henry
APPLICANT: Lamparski, Henry
Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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CIKRRARPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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100.0%; Pred. No. 8.2e-56;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-045-116-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 706141 MRSNFOERS SFO INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FOERS
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                 Sequence 20, Application US/10045116
Publication No. US20030026792A1
GENERAL INFORMATION:
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS
OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM INTE: DIBKECLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows
SOFTWARE: FRATESO for Windows Version 2.0b
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/10/222,479
FILING DATE: 16-Aug-2002
CLASSIFTCATION ATA:
APPLICATION NUMBER: US/09/614,495
FILING DATE: 11-Jul-2000
APPLICATION NUMBER: 09/033,333
FILING DATE: *UNKNOWNDATA:
ATTORNEY/AGENT INFORMATION:
NAME: CACHALING: OAD ATA:
NAME: CACHALING: AUKNOWNDATA:
NAME: CACHALING: AUKNOWNDATA:
NAME: CACHALING: AUKNOWNDATA:
NAME: CACHALING: OAD ATA:
REFERENCE/DOCKET NUMBER: 40,130
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                            CLKRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CLKRRRARPPIYRPIIVLNPHNBKIHRLDGLKPCSLLLQYD 101
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                                                                       61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD
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FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                             Sequence 22, Application US/10222479 Publication No. US20030091538A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 101 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                               Henderson, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relephone: 650-813-5600
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TELEX: 706141
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                                                                                                                                                                                                                                                                                                APPLICANT: Yu, De Chao
Schuur, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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Best Local Similarity 100.
Matches 101; Conservative
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US-10-222-479-22
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Length 95;

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WS-10-425-115-271104

Sequence 271104, Application US/10425115

PUBLication No. US20040214272A1

FRUBLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yorigwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (53222) B

CURRENT APPLICATION NUMBER: US/10/425,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/10608538
| Sequence 33, Application No. US2005064389A1
| Sequence 33, Application No. US2005064389A1
| GENERAL INFORMATION:
| APPLICANT: TORDO, NOEL
| APPLICANT: BALLOUK, CHORNE
| APPLICANT: BALLOUK, CHORNE
| APPLICANT: BALLOUK, CHORNE
| TITLE OF INVENTION: CHIMERIC LYSSAVIRUS NUCLEIC ACIDS AND POLYPEPTIDES
| FILE REFERENCE: 03495-0188-00000
| CURRENT APPLICATION NUMBER: US/09/549,519
| PRIOR PLIING DATE: 2003-06-30
| PRIOR PLIING DATE: 1999-04-14
| PRIOR PLIING DATE: 1999-04-15
| NUMBER OF SEQ ID NOS: 40
| SEQ ID NO 33
| LENGTH: 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APTIDYRNITATGLISALNIPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLICCLKRRR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 LNLPQVHAFVNDWASLDMW---WFSIALM-----FVCLIIMWLICCLKRRRARPPIYRP 74
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                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                   94.7%; Score 522; DB 5; 1
100.0%; Pred. No. 1.7e-52;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 ARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 95
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/392,822
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 95; Conservative
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                                                                                                                                                                                 TYPE: PRT
ORGANISM: Adenovirus
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Publication No. US20050169890A1
GENERAL INFORMATION:
APPLICANT: Yu, De Chao
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
FILE REFERENCE: CELL-014; 122.1
CURRENT APPLICATION NUMBER: US/0/938,227
CURRENT FILING DATE: 2004-09-09
PRIOR APPLICATION NUMBER: 60/099,791
                                                                                                                                                                                                                                                                                   1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                                                                                                                                                                              Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence II. Application US/10822873
; Publication No. US20040241857A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Henderson, D.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
FILE REPERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; CURRENT FILING DATE: 2004-04-13
; PRIOR PILICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR PILING DATE: 1998-09-10
; PRIOR PILING DATE: 1998-06-26
; PRIOR FILING DATE: 1996-06-26
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ IN DOS: 71
; SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                               61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                              100.0%; .Score 551; DB 4;
100.0%; Pred. No. 8.2e-56;
tive 0; Mismatches 0;
                                                                                                 ; OTHER INFORMATION: Amino acid sequence for ADP US-10-691-045-18
                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                              Matches 101; Conservative
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Best Local Similarity
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US-10-822-873-11
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LENGTH: 101
  LENGTH: 101
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 271104
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Zea may8
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_178843C.1.pep
US-10-425-115-271104

Query Match
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TITLE OF INVENTION: Meningococcal Antigens
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; ORGANISM: Homo sapiens
US-10-987-663-4
 RESULT 2
US-11-212-443-174
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US-10-987-663-4
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Sequence 1199, Ap
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Sequence 360, App
Sequence 5542, Appli
Sequence 510, Appl
Sequence 64, Appl
Sequence 64, Appl
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Sequence 111, Appl
Sequence 16, Appl
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Sequence 175, App
Sequence 9, Appli
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(without alignments)
113.725 Million cell updates/sec
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                                                                                                                                                                                                          1 MTGSTIAPTTDYRNTTATGL......NEKIHRLDGLKPCSLLLQYD 101
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(cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

(cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

(cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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               GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-613-7443-1199

US-10-966-648-2

US-10-966-648-2

US-10-966-648-2

US-10-966-648-2

US-11-139-443-186

US-11-139-443-186

US-11-212-443-141

US-11-212-443-141

US-11-052-554A-141

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APPLICANT: RATON, DANIEL L.

APPLICANT: WRANIK, BERND

APPLICANT: WRANIK, BERND

APPLICANT: O'YANG, WEND

APPLICANT: O'YANG, WEND

APPLICANT: O'YANG, WEND

TITLE OF INVENTION: Immune Related Diseases

FILE REPERENCE: P1996R1P1-US

CURRENT APPLICATION NUMBER: US/10/987, 663

CURRENT APPLICATION NUMBER: US 60/421,236

PRIOR PLING DATE: 2002-10-25

PRIOR PLING DATE: 2002-10-25

PRIOR PLING DATE: 2003-02-19

NUMBER OF SEQ ID NOS: 10

SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 VWWFLSGSLVIVIVCSTV-GLIICVKRKPRGDVVKVIV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
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US-11-165-160-2
US-11-055-822-586
US-10-657-827-1948
US-11-148-012-2
US-10-661-426-4
US-10-661-426-13
US-10-661-426-13
US-10-081-234-1648
US-11-000-463-259
US-11-101-337-18
US-10-353-183-57
US-10-353-183-57
US-11-191-376-4
                                                                                                                                                                                                                                             US-11-191-588-4
US-10-454-437-278
US-11-174-150-29
US-11-124-368A-292
                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 174, Application US/11212443
Publication No. US20050287165A1
GENERAL INFORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Ragignani, Vega
APPLICANT: Ragignani, Vega
APPLICANT: Ragiouli, Rino
APPLICANT: Grandi, Guido
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10987663
Publication No. US20050272118A1
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
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FEATURE:
NAME: SITE
LOCATION: (166)
OTHER INFORMATION: absent or positive
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OTHER INFORMATION: absent or positive FEATURE: STE
                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: SITE
LOCATION: (101)
OTHER INFORMATION: absent or positive
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LOCATION: (163)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATION: (170)
THER INFORMATION: absent or positive
                              LOCATION: (53)..(67)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
LOCATION: (109)
OTHER INFORMATION: absent or positive
PERTURE:
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JTHER INFORMATION: absent or positive
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THER INFORMATION: absent or positive
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THER INFORMATION: absent or positive
                                                                                                                     LOCATION: (71)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                   OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                               LOCATION: (83)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (123)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCATION: (141)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WAME/KEY: SITE
GCCATION: (155)..(156)
WHER INFORMATION: absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: absent
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
LOCATION: (104)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: overlap identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.3%; Score 62.5; DB 7; Length 222; Best Local Similarity 25.2%; Pred. No. 1.4; Matches 26; Conservative 15; Mismatches 37; Indels 2
                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ORF39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 ICCLKRRRARPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 İCA------NRTVLII-----AHRLSTVKTAHRIIAMD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 175, Application US/11212443
Publication No. US20050287165A1
GENERAL INPORMATION:
APPLICANT: Scalato, Enzo
APPLICANT: Masignani, Vega
APPLICANT: Masignani, Vega
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFERENCE: CHIROL59
CURRENT APPLICATION NUMBER: US/11/212,443
CURRENT APPLICATION NUMBER: US/09/302,626
PRIOR FILING DATE: 1999-04-30
PRIOR PRILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SEQ ID NO 175
LENGTH: 222
FILE REFERENCE: CHIR0159
CURRENT APPLICATION NUMBER: US/11/212,443
CURRENT FILING DATE: 2005-08-24
PRIOR PILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-01-14
PRIOR PILING DATE: 1999-01-14
SEQ ID NO 174
SEQ ID NO 174
CENGTH: 22
TYPE: PRI CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (16)..(33)
OTHER INFORMATION: absent or positive
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (211)
; OTHER INFORMATION: place-holder
US-11-212-443-174
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (17)..(33)
OTHER INFORMATION: place-holder
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (53)..(67)
OTHER INFORMATION: place-holder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
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12 YRNTTATGLTSALNLPQVHAFV-----NDWASLDMWWFSIA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 RARP-----PIYRPIIVLNPHNEKIHRLDGLKP 93
                                                                                                                                                       17; Mismatches
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Publication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 AFVNDWASLDMW------
                                                                                                                                                       14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 21.6
Matches 21; Conservative
                                                                                                                                                                                                                                                                                     51 VCLIIMWLICC 61
                                                                                                                                                                                                                                                                                                                                71 RTLKYLWTVČC 81
                    ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-613-744-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1199
                                                                                                                           Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-821-234-1199
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  LENGTH: 1196
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Sequence 9, Application US/10613744

Publication No. US20050272093A1

GENERAL INFORMATION:
APPLICANT: The Rockefeller University
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof
FILE REFERENCE: 018512-002901US
CURRENT APPLICATION NUMBER: US/10/613.744
CURRENT PILING DATE: 1999-03-24

PRIOR FILING DATE: 1999-03-24

PRIOR FILING DATE: 1999-03-20

PRIOR PLICATION NUMBER: US 09/045,529

PRIOR PLICATION NUMBER: WO PCT/US99/06307

PRIOR APPLICATION NUMBER: WO PCT/US99/06307

PRIOR FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 42

SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 GDTVARVRELXQIRNFLTGQALTSXLDLXFSF1F----XAVMWYYSXXLTXVVLXSLXC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GSTIAPTTD---YRN-TTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWL 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 ICCLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.8%; Score 59.5; DB 7;
Best Local Similarity 25.2%; Pred. No. 3.3;
Matches 26; Conservative 13; Mismatches 39;
                    THER INFORMATION: absent or positive
                                                                                LOCATION: (197)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (203)..(204)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (209)..(212)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (216)
OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i LOCATION: (219)...(220)
i OTHER INFORMATION: absent or positive US-11-212-443-175
                                                                                                                                                                                                                                                                                     OTHER INFORMATION: absent or positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (214)
OTHER INFORMATION: absent or positive
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                                                                                                                                                       NAME/KEY: SITE
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NAME/KEY: SITE
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LOCATION:
                                                                                                                                                                         LOCATION:
OTHER INF
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Sequence 1199, Application US/10821234

Sequence 1199, Application Worl082080255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Inv.

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ genes Version 1.0

SEQ ID NO 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 APENNEKTKEFWSTYTKAQQGESNRGSDWFQFYLTFPLIFGLFILLUFFLHWRCFLRNK 123
                                                                                                                                                     11 YPSSSSSSSSVHEPKMDALIIPVTMEVPCDSRGQRWWAAFLASSMVTFFGGLFIILLM 70
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10.4%; Score 57.5; DB 6; Length 1196; 19.7%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%; Score 57; DB 6; Length 232; 21.6%; Pred. No. 6.9; tive 15; Mismatches 27; Indels
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PRIOR FILING DATE: 1997-05-15
PRIOR PEDIGACHION NUMBER: US 09/766,396
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 31
SEG ID NO 6
LENGTH: 85
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 36.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rattus sp. FEATURE:
                                                                                                                                                                         TYPE: PRT
ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-966-648-27
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                                                                                                                                                                                                                        FEATURE:
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Publication No. US20050249734A1

GENERAL INFORMATION:

APPLICANT: Sutcliffe, J. Gregor

APPLICANT: Henriksen, Steven J.

APPLICANT: The Scripps Research Institute

TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods

FILE REFERENCE: 14740A-000640US

CURRENT APPLICATION NUMBER: US/10/966,648

CURRENT FILING DATE: 2004-10-14

PRIOR APPLICATION NUMBER: US 08/648,322

PRIOR PILING DATE: 1996-05-15

PRIOR PILING DATE: 1996-05-15

PRIOR APPLICATION NUMBER: US 08/857,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 VVSSTLSPEKDSR----VSVTKPFMLPPVAASSLRNDSSSSNRKAKONPTGDSSLHWAAMA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---MWWFSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%; Score 57; DB 6; Length 273; 26.0%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHA--FVNDWASLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 L-MFVCLIIMWLICCLKRRRARPPIYRPI--IVLNPHNEKIHRL 88
                        COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 01017/32958A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.3%; Score 57; DB 6
Best Local Similarity 26.0%; Pred. No. 8.3;
Matches 27; Conservative 18; Mismatches
                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NO-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/689,701
FILING DATE: 01-CCT-1990
APPLICATION NUMBER: 07/573,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-353-783-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                                                                                                                             FILING DATE: 28-Jan-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 50:
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APPLICANT: Sutcliffe, J. Gregor
APPLICANT: Ge Lecea, Luis
APPLICANT: de Lecea, Luis
APPLICANT: de Lecea, Luis
APPLICANT: de Lecea, Luis
APPLICANT: Siggins, George
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
FILE REFERENCE: 1470A-000640US
CURRENT APPLICATION NUMBER: US 108/648,322
PRIOR APPLICATION NUMBER: US 08/648,322
PRIOR PILING DATE: 1996-05-15
PRIOR PLING DATE: 1997-05-15
PRIOR FILING DATE: 2001-118
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
: SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10966648
Publication No. US20050249734A1
Publication No. US20050249734A1
Publication No. US20050249734A1
APPLICANT: Sutcliffe, J. Gregor
APPLICANT: de Lecea, Luis
APPLICANT: Henriksen, Steven J.
APPLICANT: Siggins, George R.
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: positions 10-112 of rat preprocortistatin (CST) OTHER INFORMATION: cortistatin-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                  12;
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10.2%; Score 56; DB 6; Length 103;
Best Local Similarity 36.4%; Pred. No. 3.8;
Matches 12; Conservative 5; Mismatches 4; Indels
                                                                          DB 6; Length 85;
3;
                                                                                                                               Indels
                                                                                                                                     4
                                                                                                                                                                                                                        62 LKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPC 94
                                                                                                                                                                                    62 LKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 LSKROERPPLOOP----PHRDK-----KPC 91
                                                                             ; Score 56; DB 6
; Pred. No. 3;
5; Mismatches
, OTHER INFORMATION: rat procortistatin US-10-966-648-6
                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/10966648
Publication No. US20050249734A1
GENERAL INFORMATION:
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                       CURRENT APPLICATION NUMBER: US/10/454,437

CURRENT FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: US 60/141031

PRIOR PILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR PLILING DATE: 1999-07-19

PRIOR PLILING DATE: 1999-07-14

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.2%; Score 56; DB 6; Length 1274; Best Local Similarity 20.2%; Pred. No. 59; Matches 18; Conservative 21; Mismatches 28; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: POTZAN Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNAI Vega
APPLICANT: MASIGNAI Vega
APPLICANT: MASIGNAI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVERTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PILICATION NUMBER: GB-0103424.8
PRIOR APPLICATION VERBION 1.04
SCOUTHARE: SeqWin99, VerBion 1.04
SEQ ID NO 5542
LENGTH: 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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Pred. No. 5.5;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1110 ITVVWKW-VCVGKHKPSEHPLFSRFVWLN 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 VCLIIMWLICCLKRRRARPPIYRPIIVLN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Corynebacterium glutamicum US-10-454-437-360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5542, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
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US-10-467-657-5542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 27.5%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-467-657-5542
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Publication No. US20050277115A1

GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 LIIMWLICCLKRRRARPPIYRPIIVLNPHNE-----KIHR--LDGLKPCSLLL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%; Score 56; DB 6; Length 112; 36.4%; Pred. No. 4.1; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fann, Ming-Ji
TITLE OF INVENTION: Cellular Proliferation Control Factors
FILE REPERENCE: 1741-002001
CURRENT APPLICATION NUMBER: US.011/139,435
CURRENT FILING DATE: 2005-05-27
RICH PRIOR FILING DATE: 2004-05-27
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 LKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPC 94
FILE REFERENCE: 14740A-000640US
CURRENT APPLICATION NUMBER: US/10/966,648
CURRENT FILING DATE: 2004-10-14
PRIOR APPLICATION NUMBER: US 08/648,322
PRIOR APPLICATION NUMBER: US 08/657,389
PRIOR FILING DATE: 1996-05-15
PRIOR PRILING DATE: 1997-05-15
PRIOR PRILING DATE: 1997-05-15
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: rat preprocortistatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/11139435; Publication No. US20050287664A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SIGNAL
LOCATION: (1)...(27)
CHER INFORMATION: signal peptide
US-10-966-648-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 36.47
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Best Local Similarity 30.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: M. musculus
US-11-139-435-2
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-10-454-437-360
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LENGTH: 1191
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US-11-139-435-2
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US-11-052-554A-141

; Sequence 141, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION:
}
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117 TGSTVSSPEGRNTVTAKXIDVEFANNRYATDYAHTQEQKGLTVALNVPVVQAAQN 171
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Pred. No. 34;
                                                                         221 LPAFFSLVIGFAFGALYWKKKQPNLTRTVENIQINEEDNEISML 264
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                               48 L-MFVCLIIMWLICCLKRRRARPPIYRPI--IVLNPHNEKIHRL
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Scalato, Enzo
APPLICANT: Masignani, Vega
APPLICANT: Masignani, Vega
APPLICANT: Pizza, Mariagrazia
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FIEB REFERENCE: CHIROLS9
CURRENT APPLICATION NUMBER: US/11/212,443
CURRENT APPLICATION NUMBER: US/09/3302,626
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SOFTWARE: PATENTING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
TYPE: PRI
TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4, Mismatches
                                                                                                                                                                                                                                                             Sequence 64, Application US/11212443 Publication No. US20050287165A1 GENERAL INFORMATION:
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Best Local Similarity 32.7%;
Matches 18; Conservative
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; OTHER INFORMATION: unknown
US-11-212-443-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (64)..(65)
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: SITE
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LOCATION: (232
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTGSTIAPTTDYRNTTATGLISALNLPQVHA--FVNDWAS------LDMWWFSIA 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 24-Jan-2003
CLASSIFICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/48,729
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-OCT-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 10-OCT-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 10-OCT-1999
APPLICATION NUMBER: 07/537,198
FILING DATE: 10-OCT-1999
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W:
REGISTRATION NUMBER: 36,107
FELERHOUR: 312/44.6300
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Sequence 51, Application US/10353783;
Publication No. US20050261175A1
GENERAL INPORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Sugge, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-353-783-51
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TOPOLOGY: linear
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 25.09
Matches 26; Conservative
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Copyright (c) 1993 - 2006 Compugen Ltd.
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32 72 13.1 218 2 0723K1 HUMAN Q723K1 homo sapien G37535 Karharina t G475 12.9 283 1 TWR14 HUMAN G4595 Karharina t G6GNB1 Karharina	SULT 1 E311_ADE02 E311_ADE02 E313_ADE02 STANDARD; PRT; 101 P24935; 01-MAR-1992 (Rel. 21, Created) 01-MAY-1992 (Rel. 21, Last sequence upda 10-MAY-2005 (Rel. 47, Last annotation up Early E3A 11.6 Kba glycoprotein. Human adenovirus 2 (HAdV-2). Viruses; dabNA viruses, no RNA stage; Ad	NCBL TaxID=10515, [1] NUCLBOTIDE SEQUENCE. MEDLINE=81053687; PubMed=65, Herisse J., Courtois G., Gg "Nucleotide sequence of the Nucleic Acids Res. 8:2173-7 [12] IDSTIFICATION OF PROTEIN. MEDLINE=93079877; PubMed=125071877; PubMed=115071877; PubMed=125071877; PubMed=125071877; PubMed=125071877; PubMed=125071877; PubMed=125071877; PubMed=125071877; PubMed=125071877; PubMed=125071877; PubMed=12507187; PubMed=1	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed. EMBL, J01977, AAA92222.1; -; Genomic_DNA. InterPro; IPR008652; Hum_adeno_E3A. Party Protein; GlyCoprofein; Transmembrane. TRANSMIM 41 62 Potential. CARBOHYD 14 14 N-linked (GLOAC) (Potential).	Query Match Best Local Similarity 100.0%; Score 551; DB 1; Batches 101; Conservative 0; Mismatches I MTGSTIAPTIDYRNITATGLTSAINLPQVHAFVNDWAS
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11.6K protein.
Human adenovirus 2 (HAdV-2).
Viruses; debNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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Submitred (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ2991915, CAG67721.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR008652; Hum adeno E3A.
Pfam; PF05593; Hum adeno E3A.
SEQUENCE 101 AA: 11662 MW; 914F50AC2F8B284F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FB89FCC6E921E84B CRC64;
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         101 AA
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EMBL; AJ293916; CAC67713.1; -; Genomic DNA.
EMBL; AJ293917; CAC67729.1; -; Genomic DNA.
EMBL; AJ29312; CAC6786.1; -; Genomic DNA.
GO; GO:0016021; C:Integral to membrane; IEA.
InterPro; IPR086652; Hum adeno E3A.
EEGUENCE 101 AA; 11644 MW; FB89FCC6E9211
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Human adenovirus 2 (HAdV-2)
Q779E8 ADE02 PRELIMINARY;
Q779E8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MIGSTIAPTIDYRNITATGLIFALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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Reichmann H., Schaarschmidt E., Geieler B., Hausmann J., Ortmann D.,
Bauer U., Plunker G., Seidel W.;

Bauer U., Plunker G., Seidel W.;

"Sequence analysis of group C human adenoviruses type 1 and 6 for five
genes of region E3.";

Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

-1- SUBCELLULAR LOCATION: Integral nuclear membrane protein.

-1- PTM: N-glycosylated and probably also O-glycosylated (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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RESULT 4

091246_ADE02

LD 091246_ADE02 PRELIMINARY; FRT; 101 AA.

AC 091246.

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DCT-2003 (TrEMBLrel. 25, Last annotation update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

COT-2003 (TrEMBLrel. 25, Last annotation update)

OC Viruses; denovirus 2 (HAdv-2).

OC Viruses; denoviruses, no RNA stage; Adenoviridae; Mastadenovirus.

ON NCBI_TAXID=10515;
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NCBI_TaxID=10534;
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InterPro; IPR008652; Hum_adeno_E3A.

Pfam; PF05393; Hum_adeno_E3A; 1.

Early protein; Glycoprotein; Transmembrane.

TRANSMEM 41 62 Protential.

CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).

SEQUENCE 101 AA; 11613 MW; EF219000939E3B4B CRC64;
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-!- SIMILARITY: Belongs to the adenoviruses E3A-1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borcherding F., Pring-Akerblom P.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ293913; CAC67704.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPRO08652; Hum_adeno_E3A.
Ffan; PF05393; Hum_adeno_E3A, I.
SEQUENCE 101 AA; 11704 MW; E13857DC5891E85B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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98.9%; Score 545; DB 2;
Best Local Similarity 99.0%; Pred. No. 4.8e-52;
Matches 100; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Early E3A 11.6 kDa glycoprotein.
Human adenovirus 6 (HAdV-6).
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TISSUE=Liver;
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MIGSTIAPTTDYRNTTATGLKSALNLPQVHAFVNDWASLGMWWFSIALMFVCLIIMMLIC 60
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                                                                             1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Hannover /Adrian German reference center for adenoviruses, setchmann H., Schaarschmidt E., Geisler B., Hausmann J., Ortmann D. Bauer U., Flunker G., Seidel W. Sedies W. Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human adėmovirus 1 (HAdV-1).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Hannover /Adrian German reference center for adenoviruses, Reichmann H., Schaarschmidt E., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Natural variation among human adenoviruses: genome sequence and annotation of human adenovirus serotype 1.";
J. Gen. Virol. 85:2615-2625(2004).
EMBL; V11257; CAA71217.1; -; Genomic_DNA.
EMBL; V11032; CAA71216.1; -; Genomic_DNA.
EMBL; AF534906; AAQ10560.1; -; Genomic_DNA.
EMBL; AF534906; AAQ10560.1; -; Genomic_DNA.
EMBL; AF534906; AAQ10560.1; -; Genomic_DNA.
EMBL; PR05393; Hum_adeno_E3A.
From PP05393; Hum_adeno_E3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
PubMed=15302955; DOI=10.1099/vir.0.80118-0;
Lauer K.P., Llorente I., Blair E., Seto J., Krasnov V.,
Purkayastha A., Ditty S.E., Hadfield T.L., Buck C., Tibbetts C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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97.6%; Score 538; DB 1; Length 101; 98.0%; Pred. No. 2.8e-51; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 355; DB 2; Length 94;
Pred. No. 3.8e-31;
8; Mismatches 9; Indels
                                                                                                                                                       61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                           CLKGRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLLQYD 101
                                                                                                                                                                                                                                                                                                                         01-JUJ-1997 (TrEMBLrel. 04, Created)
01-JUJ-1997 (TrEMBLrel. 04, Last sequence update)
01-FEB-2008 (TrEMBLrel. 29, Last annotation update)
11.6K protein (10.7 kDa protein).
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Last annotation update)
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(Rel. 15, Last sequ
(Rel. 47, Last anno
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                                     99; Conservative
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NUCLEOTIDE SEQUENCE.
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                     Best Local Similarity
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Best Local Similarity
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01-AUG-1990
10-MAY-2005
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E311_ADE05
ID E311_ADE05
AC P175\(\begin{array}{c}
0.1-AUG-1990\)
DT 10-MAY-2005
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Query Match
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 NITNAAAAIGLISITNIPQVSAFVNNWDNLGMWWFSIALMFVCLIIMWLICCLKRKRARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 NTT----ATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLICCLKRRARRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                               MEDLINE-22087470; PubMed=1727603; Chroboczek J., Bieber F., Jacrot B.; The sequence of the genome of adenovirus type 5 and its comparison with the genome of adenovirus type 2."; Virology 186:280-285[1992].
-- SUBCELLULAR LOCATION: Integral nuclear membrane protein.
-- PTM: N-glycosylated and probably also 0-glycosylated.
-- SIMILARITY: Belongs to the adenoviruses B3A-1 family.
                                                                                                                                               adenovirus 5.";
Barly E3A 10.5 kDa glycoprotein.
Human adenovirus 5 (HAdV-5).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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NCBI_TaxID=129951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McAllister D.L., Lu F., Thomas B.K., Hutchins B.M., Sugarman B.J.; "Complete Nucleic Acid Sequence of the Adenovirus Type 5 Reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-linked (GlcNAc. . .) (Potential) 008AD087AAB45A8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 93;
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GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPRO08652; Hum_adeno_E3A.
Pfam; PF05393; Hum_adeno_E3A; 1.
SEQUENCE 93 AA; 10523 MW; 008AD087AAB45A8F CRC64;
                                                                                                    MEDLINE-85092388; PubMed=2981456;
Cladaras C., Wold W.S.M.;
"DNA sequence of the early E3 transcription unit of
Virology 140:28-43(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGVGT8 9ADEN PRELIMINARY; PRT; 93 AA.
QGVGT8;
QGVGT8;
GCJUL-2004 (TrEMBLrel. 27, Created)
O5-UUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M73260; -; NOT ANNOTATED CDS; Genomic_DNA.
EMBL; X03002; CAA26784.1; -; Genomic_DNA.
PIR; A05245; ERAD53.
InterPro; IPR008652; Hum_adeno_E3A.
Pfan; PF05393; Hum_adeno_E3A; I.
Early protein; Glycoprotein; Transmembrane.
TRANSMEM 34 55
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.8%; Score 346; DB 1;
78.3%; Pred. No. 3.7e-30;
tive 6; Mismatches 8
                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA)
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                                                                                           NUCLEOTIDE SEQUENCE.
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                                                       NCBI_TaxID=28285;
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Q6VGT8_
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Indels

Length 276;

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Query Match
19.5%; Score 107.5; DB 2;
Best Local Similarity 28.8%; Pred. No. 0.0021;
Matches 23; Conservative 21; Mismatches 23;
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255 YFVCCKAREKSRRPIYRPVI 274
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Q76ELS;
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QSTIZ2;
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PubMed=12560390; DOI=10.1136/jcp.56.2.120;
Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukouyama A., Matsuno S.,
Inada T., Okabe N.;
"Genetic Characterization of Adenovirus Type 8 Isolated in Hiroshima
City over a 15-year Period.";
J. Clin. Pachol. 56:120-125(2033).
EMBL; AB097769; BAC58004.1; -; Genomic_DNA.
SEQUENCE 276 AA; 30919 MW; 587D4C95AE86BC26 CRC64;
                                                                                                                                                                                                                                    14 NTT----ATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLICCLKRRRARP
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STRAIN=8P prime;
STRAIN=8P prime;
PubMed=12560390; DOI=10.1136/jcp.56.2.120;
Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukouyama A., Matsuno S.,
Inada T., Okabe N.;
"Genetic Characterization of Adenovirus type 8 Isolated in Hiroshima City over a 15-year Period.";
J. Clin. Pathol. 56:120-125 (2003).
EMBL; AB110079; BAC82700.1; -; Genomic_DNA.
SEQUENCE 276 AA; 30879 MM; 838596E7F65BBEEE CRC64;
                                                                                                      Gaps
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
A5 protein
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Human adenovirus type 8E.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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Human adenovirus 8 (HAdV-8).
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=31545;
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62.8%; Score 346; DB 2; Length 93; 78.3%; Pred. No. 3.7e-30; ive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q76C86 ADE08 PRELIMINARY; PRT; 276 AA. Q76C86. Q76C86. CF-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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235 YFVCCKAREKSRRPIYRPVI 254
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Q80IV7;
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PubMed=12560390; DOI=10.1136/jcp.56.2.120;
Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukouyama A., Matsuno S.,
Inada T., Okabe N.,
"Genetic Characterization of Adenovirus type 8 Isolated in Hiroshima
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=31545;
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Viruses; dsDNA viruses, no RNA stage; Ademoviridae; Mastademovirus.
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Buettner W.H., Veres-Molnar S.K.;
"Adenovirus type 9, complete sequence.";
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ854486; CALGS981.1; -; Genomic DNA.
SEQUENCE 296 AA; 33125 WW; 256ED64914353439 CRC64;
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J. Clin, Pathol, 56:120-125 (2003).
EMBL, AB106356; BAC87854.1; , 26comic DNA.
SEQUENCE 261 AA; 29415 MW; 91433010DAA306B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEE-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
E3 orf3 33.1 kba protein.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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completed: January 18, 2006, 19:47:55
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Matches 26; Conserva
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                                                                         2 TGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLICC
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PubMed=12560390; DOI=10.1136/jcp.56.2.120;
Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukouyama A., Matsuno S.,
Inada T., Okabe N.;
"Genetic Characterization of Adenovirus Type 8 Isolated in Hiroshima
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=31545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 18.2%; Score 100.5; DB 2; Length 281; Local Similarity 26.2%; Pred. No. 0.012; les 21; Conservative 22; Mismatches 24; Indels 13;
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                         34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome Sequence of Human adenovirus type 46.";
Submitred (DEC-2004) to the EMBL/Genbank/DDBJ databases.
EMBL; AY875648; AAX10939.1; -; Genomic DNA.
SEQUENCE 281 AA; 30918 WW; 23CF181230DA2032 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78834.1; -; Genomic DNA.
29138 MW; D3742E9ADBAC5CF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                               281 AA
  Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 AA
Best Local Similarity 24.0%; Pred. No. 0.01 Matches 18; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           City over a 15-year Period.";
J. Clin. Pathol. 56:120-125(2003).
EMBL; AB102672; BAC78834.1; -; Genc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 YFVCCKAREKSRRPIYRPVI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLICCLKRRRARPPIYRPII 76
                                                                                                                                                                                                 |:::| |||||:|
225 KARKKSRRPIYRPVI 239
                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                       62 LKRRRARPPIYRPII 76
                                                                                                                                                                                                                                                                                            19_9ADEN
Q4KSI9_9ADEN PRELIMINARY;
Q4KSI9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7TBG9_ADE08 PRELIMINARY;
Q7TBG9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=46941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Police S.R.;
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OTTEGS ADE
DE 077EG
DT 01-0C

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141 TTAAPTTAAATTQSSHVNKDICMPSSEPGTSSENILNLYCEIFIWAPL----AGVCLVLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 STIAPTTDYRNTTATGL-----TSALNLPQVHAFVNDWASLDMWWFSIALMFV 51
                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CD8 alpha chain precursor.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tregaskes C.A., Kong P.K., Paramithiotis E., Chen C.1.H.,
Ratcliffe M.J.H., Davison T.F., Young J.R.;
Ratcliffe M.J.H., Davison T.F., Young J.R.;
"Identification and analysis of the expression of CD8 alpha beta and CD8 alpha alpha isoforms in chickens reveals a major TCR-gamma delta CD8 alpha beta subset of intestinal intraepithelial lymphocytes.";
J. Immunol. 154:4485-4494(1995).
EMBL; Z22726; CAA80421.1; -; mRNA.
BIR; ISO610; ISO610.
Ensembl; ENSGALGGOO00015816; Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 14.0%; Score 77; DB 2; Length 235; 1 Similarity 25.2%; Pred. No. 4; 26; Conservative 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 CLIIMWLICCLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 CD8 alpha chain.
26100 MW; 525326EE1AA4B512 CRC64;
                                                                                                                                                                                                                                                                                                                            235 AA
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                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                       218 YFVCCKTKKKSRRPIYRPVI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=RPL line 7; TISSUE=Spleen; MEDLINE=95238946; PubMed=7722305;
                                                                                                   57 WLICCLKRRRARPPIYRPII 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003599; IG.
InterPro; IPR000110; Ig-like.
Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG, LIKE; 1.
Immunoglobulin domain; Signal, SIGNAL.
                                                                                                                                                                                                                                                                                                            Q90770 CHICK PRELIMINARY;
Q90770;
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us-10-822-873-11.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 18, 2006, 19:43:21; Search time 16 Seconds (without alignments) 607.368 Million cell updates/sec

US-10-822-873-11 551 1 MTGSTIAPTTDYRNTTATGL.....NEKIHRLDGLKPCSLLLQYD 101 Title: Perfect score:

Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	3A 10.5K	T-cell surface gly	disintegrin (EC 3.	NADH2 dehydrogenas	۲.	disintegrin (EC 3.		_	hypothetical prote		hypothetical prote		transmembrane glyc	hypothetical prote				hypothetical prote	copper resistance	hypothetical prote	protein-tyrosine k	protein-tyrosine k	multidrug-efflux t	probable membrane	protein F21D18.14	hypothetical prote	О	hypothetical prote	hypothetical prote
SUMMARIES	ID	ERAD53	150610	S52477	850336	T01316	S66129	872597	AG0784	AH2409	T28767	T19413	S52920	A46103	T19416	T48284	T22046	T19412	S42125	S52258	T22922	I48696	148697	G69804	T36483	E96521	F87652	T14339	2	T15863
	DB	-	~	~	~	~	~	7	N	~	~	~	~	~	~	~	~	~	~	~	~	-	٦	н	~	~	~	~	~	N
	Query Match Length	93	235	544	316	324	748	95	518	429	340	1187	491	522	533	428	244	306	279	466	242	871	881	518	83	150	254	0	638	1667
مد	Query	62.8	14.0	n	m	12.7	12.7	N	N	$^{\circ}$	12.3	N	12.2	2	2	12.1	12.0	11.9	11.8	11.8	11.7	11.7	11.7	11.6	11.5	11.5	11.5	11.5	11.5	11.5
	Score	ا س	77	74	72	70	70	69.5	69.5	68	67.5	67.5	67	67	67	66.5	99	65.5	65	65	64.5	4	64.5	64	63.5	63.5	ë.	63.5	۳.	63.5
	Result No.		8	М	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	53

UL73 glycoprotein large surface anti	SSUI protein - yea hypothetical prote	hypothetical prote protein W06E11.6 [probable membrane TRK potassium upta	hypothetical prote hypothetical prote	exopolysaccharide El membrane glycop	hypothetical prote mating-type locus	b3 protein - smut protein T6D22.10 [
QQBEB2 S67506	S61974 C70597	T00529 E88382	T02789 E84324	F82493 AH1148	S74742 S47427	T15964 C36671	D32696 B86215
7 7	0 0	0 0	0 0	0 0	0 0	~ ~	0 0
138	458	844	332 558	162 256	756 262	283	410
11.4	11.4	11.4	11.3	11.3	11.3	11.2	11.2
63	89	63 62.5	62.5 62.5	62 62	62 61.5	61.5	61.5
30	33	3.4 3.5	36	38 39	40	42	44

ALIGNMENTS

RESULT

-	ERAD53	
	early E3A 10.5K prot	early E3A 10.5K protein - human adenovirus 5
	A: Note: host Homo saniens (man)	ullan adenovitus
	C;Date: 31-Mar-1990	C.Date: 31-Mar-1990 #Bequence revision 31-Mar-1990 #text_change 09-Jul-2004
	C, Accession: A05245	
	Nicologians, C.; Wold, W.S.M.	מי איני.אי.
	A; Title: DNA sequence	A.F.Ttele: DNA sequence of the early E3 transcription unit of adenovirus 5.
	A; Reference number:	A.Reference number: A94335, MUID:85092388; PMID:2981456
	A; Accession: A03243	4
	A; Residues: 1-93 <cla></cla>	LA>
	A;Cross-references: C;Superfamily: adenc	A;Cross-reterences: UNIPROT:P17590; UNIPARC:UP10000037966; GB:X03002; NID:G58503; FIDN:C3 C;Superfamily: adenovirus early E3A 10.5K protein
•	C, Keywords: early pr	C;Keywords: early protein; transmembrane protein
	Query Match Best Local Similarity Matches 65: Conserv	h 62.8%; Score 346; DB 1; Length 93; Similarity 78.3%; Pred. No. 6.2e-31; 65: Conservative 6; Mismatches 8; Indels 4; Gaps 1;
	14 NTT	J.POVHAFVNDWASI.DMWWFSIALMFVCLIIMWLIC
-	Db 3 NTTNA	DNLGMWWFSIALMFVCLIIMWLICCLK
	Oy 70 PIYRPI	PIYRPIIVLNPHNEKIHRLDGLK 92
_	;	
	Db 63 PIYSPI	PIYSPIIVLHPNNDGIHRLDGLK 85
	RESULT 2	
	150610	
	T-cell surface glyco	T-cell surface glycoprotein CDB alpha chain - chicken
	C;Species: Gallus gallus (cnicken)	allus (chicken) #semience revision 13-Sen-1996 #text change 09]11]-2004
	C; Accession: I50610;	Cibaccession: IS6610; S33350
	R, Tregaskes, C.A.; I	R,Tregaskes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison,
	A.Title: Identificat	. Immunioli. 154, 4485-4494, 1955 b.mitle. Identification and analysis of the expression of CDR alpha heta and CDR alpha a
	ymphocytes.	
	A:Reference number:	A, Reference number: 150609; MUID:95238946; PMID:7722305
	A; Accession: I50610	a track (and the control of the con
	A:Status: preliminary	AfsCatus: preliminary; translated from GB/EMBL/DUBJ b.MJ ecula from . mbWz
	A;Residues: 1-235 <tre></tre>	TRE>
	A; Cross-references:	A;Cross-references: UNIPROT:Q90770; UNIPARC:UP100000FBABF; EMBL:222726; NID:G488149; PIDN
	C;Superfamily: immunoglol	C;Superfamily: immunoglobulin V region; immunoglobulin homology earborde: alvonvotei
	civerwords: gricopic	

14.0%; Score 77; DB 2; Length 235; 25.2%; Pred. No. 0.55;

Query Match Best Local Similarity

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A,Molecule type: DNA
A,Residues: 1.-324 «KAL»
A,Cross-references: UNIRROT:081299; UNIPARC;UPI00000AC70B; EMBL:AF069298; NID:g3193282; E.
A,Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-748 cGLY-
A;Cross-references: UNIRROT:Q10741; UNIPARC:UPI00001254C7; EMBL:Z21961; NID:g1044810; PII
A;Note: this is a revision to the sequence from reference S32205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, March 1993
A;Description: Identification of a mammalian member of the metalloproteinase/disintegrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the metalloproteinase/disintegrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 GLIDSLGVDRVFLVGHDWGAIVAWW-------LCMIRPDRVN-ALVNTSVVF 128
                                                                                                                                                                                                                                                                                                                                         C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   distincegrin (EC 3.4.24.-) precursor - bovine C; Species: Bos primigenius taurus (cattle) Si2008 Si2208 Si2208 Si2208 Si2008 Si2208 Si22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 GLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLICCLKRRRARPPIYRPIIVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule type: mRNA

A Mesidues: 1-13,'LAM',117,'LILMEDLKDSFRLMVAR',135-171,'R',173-652,'L'

A) Residues: 1-13,'LAM', 117,'LILMEDLKDSFRLMVAR',135-171,'R',173-652,'L'

A) Note: this sequence has been revised in reference S66129

CKEYWORDS: hydrolase; metalloproteinase; zinc

F) 1-13/Domain: signal sequence #status predicted <SIG>

F) 1-13/Domain: signal sequence #status predicted <AT>

F) 1-13/Domain: disincegrin homology <OIS>

F) 383,387,393/Binding site: zinc, catalytic (His) #status predicted F) 384,Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70; DB 2; Length 748; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29; Indels
                                                                                                                                                                                                                                                                                            epoxide hydrolage homolog T14P8.15 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T01316
R;Kailcki, J.; Bliott, G.; Cloud, J.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of A. thaliana T14P8.
A;Reference number: Z14290
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.7%; Score 70; DB 2
Best Local Similarity 20.3%; Pred. No. 4.4;
Matches 15; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%;
23.7%;
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129 NPRNPSVKPVDAFR 142
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                                                     :: ||
188 IVVCLAETNRAP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 4
A;Introns: 155/3; 235/2
A;Note: T14PB:15
C;Superfamily: tropinesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S32205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disintegrin (EC 3.4.24.-) precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Baccies: S2477
R;HOward, L:, Mitchell, S; Lu, X:, Griffiths, S.; Glynn, P.
R;Howard, L:, Mitchell, S.; Lu, X:, Griffiths, S.; Glynn, P.
R;Howard, L:, Mitchell, S.; Lu, X:, Griffiths, S.; Glynn, P.
R;Howard, L:, Mitchell, S.; Lu, X:, Griffiths, S.; Glynn, P.
R;Howard, L:, Mitchell, S.; Lu, X:, Griffiths, S.; Glynn, P.
R;Howard, L:, Mitchell, S.; Lu, X:, Griffiths, S.; Glynn, P.
A;Hoescription: Molecular cloning of MADM: a catalytically-active mammalian disintegrin-m
A;Reference number: S52477
A;Molecule type: mRNA
A;Residues: 1-544 cHOW.>
A;Residues: 1-544 cHOW.>
A;Residues: 1-544 cHOW.>
A;Cross-references: UNIPROT:Q10743; UNIPRAC:UPI00001254CA; EMBL:Z48444; NID:g683662; PIC
C;Reywords: hydrolase; metalloproteinase; transmembrane protein; zinc
F;10-544/Product: disintegrin homology cNIS>
F;252-342/Domain: signal sequence (fragment) #status predicted cNM>
F;252-342/Domain: transmembrane #status predicted cTMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Katharina tunicata mitochondrion C.Species: mitochondrion Katharina tunicata C.Species: mitochondrion Katharina tunicata C.Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C.B.Boore, J.L., Brown, W.M. A.Boore, J.L., Brown, W.M. A.M. M.M. A.Speciesion: 319, 423-443, 1994 A.Title: Complete DNA sequence of the mitochondrial genome of the black chiton, Katharin A.Reference number: S50327; MUID:95129806; PMID:7828825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-316 <BCO>
A;Cross-references: UNIPROT:Q37535; UNIPARC:UPI000092089; EMBL:U09810; NID:g557273; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: ND1
A;Genome: mitochondrion
A;Genome: mitochondrion
A;Genome: mitochondrion
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit phosphorylation;
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                                                                                                                                              --TSALNLPQVHAFVNDWASLDMWWFSIALMFV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IGSTI----APTIDYRN-----TIATG----LISALNLPOVHAFVNDWASLDMW 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 IAPTIDYRNT-----TATGLTSALNLPQV--HAFVNDWASLDWWWFSIALMFVCLIIMW 57
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.1%; Score 72; DB 2; Length 316; 27.8%; Pred. No. 2.6;
18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                                                                                                                                                                                                                                                   52 CLIIMWLICCLKRRARPPIYRPIIVLNPHNEKIHRLDGLKPC 94
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                                                                                    4 STIAPTTDYRNTTATGL--
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    26; Conservative
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hypothetical protein all4832 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. et 7120
C;Species: Nostoc sp. et 7120
C;Species: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2409
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Natanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
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CjSpecies: Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjAccession: T28767
RjRohlfingy T.; Wohldmann, P.
RjRohlfingy T.; Clone W03D2
AjExperimental Bource: Strain Bristol N2; clone W03D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8YMU5; UNIPARC:UPI0000CEC7A; GB:BA000019; PIDN:BAB76531.1; A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 GLVEVLTLPERVIHASGASVYLFVDSFLRYEKWIANPLAALYACSFALCITLL----AS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30
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C;Species: Caenorhabditis elegans
C;Pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19413
R;Wilkinson, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 TWFKQWYAVDLIWAIAAALIMGFVVAKAIVWIDQKVQKRRSADALMBDFIALS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 AFVNDWASLDMWWFSIALMF----VCLIIMWLICCLKRRARPPIYRPIIVLN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.3%; Score 67.5; DB 2; Length 340; Best Local Similarity 25.0%; Pred. No. 8.7; Matches 21; Conservative 16; Mismatches 30; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTGSTIAPT-----TDYRN------TTATGLTSALNLPQVH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 12.3%; Score 68; DB 2; Length 429; Similarity 21.2%; Pred. No. 9.8; 24; Conservative 19; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 4
A;Introns: 63/3; 118/2; 185/3; 210/3; 253/3; 314/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 PPIYRPIIVLNPHNEKIHRLDGLK 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-429 <KUR>
                                                                                                                                                                                                                                                                                                                           A;Accession: AH2409
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Atthors: Parry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Atthors: A80502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:Q49760; UNIPARC:UP10000139B2E; EMBL:U00016; NID:g466961; PID
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                                                                                                         203 TVAELPGTPSRQATINGLPLKIQL----YADSWTYNDLWY---ALMLGCISGIVAGFIC 254
                                                                 ----TTATG----LTSALNLPQVHAFVNDWASLDMWW 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 TIA--PITDYRNITATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCL--IIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                      Nypothetical protein B1937 F2_47 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Accession: S72597
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Reference number: S72580
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                                                                                                                                                                                                                               ::: || : ||:: ||: || 679 WAVLLMGIALIMLWAGFIKICSVHTPSSNPKLPPPKPLPGTLKRRRPPQPIQQP 732
                                                                                                                                                                                              74
                                                                                                                                                                                              ---CLKRRRARPPIYRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 TVFYDAGTANG-TNGISVSPVNGFLNWWDSIELWLSGLAFVLQAALVM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 69.5; DB 2; Length 95; 29.2%; Pred. No. 1.5;
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   26; Indels
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; Pred. No. 8.1;
13; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 YFIYALKTRÞGKEILTAIKHEOFYVVÝOÞVV 285
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      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Superfamily: probable membrane protein ylaB
   17;
                                                                                                                                                                                           44 FSIALMFVCLIIMWL----IC
                                                                 3 GSTI-----APTTDYRN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%;
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   27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 -CLKRRRARP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-518 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
      Matches
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AH2409
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C,Accession: A46103; D46104
R,Tordo, N.; Bourhy, H.; Sather, S.; Ollo, R.
Virology 194, 59-69, 1993
A,Title: Structure and expression in baculovirus of the Mokola virus glycoprotein: an eff.
A,Reference number: A46103; WUID:93242783; PMID:8480429
A,Accession: A46103
                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: 1-522 <TOR>
A;Residues: 1-522 <TOR>
A;Residues: 1-522 <TOR>
A;Cross-references: UNIPROT: Q89507; UNIPARC: UPI00000F7438; GB: S59447; NID: g299713; PIDN: J1
A;Cross-references: UNIPROT: Q89507; UNIPARC: UPI00000F7438; NCBIP: 130541)
B;Bourhy, H; Kissi, B; Tordo, N.
A;Rology 194, 70-81, 1993
A;Title: Molecular diversity of the Lyssavirus genus.
A;Caference number: A46104; MUID: 93242784; PMID: 8386891
A;Cottents: lyssavirus serotype 3
A;Accession: D46104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: genomic RNA
A;Residues: 1-522 <BOU>
A;Crose-references: UNIPARC:UPIO0000F7438; GB:S59448; NID:g299715; PIDN:AAB26296.1; PID:g:
A;Note: sequence extracted from NCBI backbone (NCBIN:130542, NCBIP:130548)
C;Superfamily: rabies virus spike glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UPI000007A484; EMBL:Z69717; PIDN:CAA93533.1; GSPDB:GN00028; C
A;Experimental source: clone E01G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 14/1; 54/1; 58/3; 125/3; 162/1; 194/1; 234/1; 295/1; 319/1; 354/2; 403/1; 455/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosduces: 1-533 «MIL»
A;Rosiduces: 1-533 «MIL»
A;Cross-references: UNIRROT:017592; UNIPARC:UPI000007A484; EMBL:278416; PIDN:CAB01683.1;
A;Experimental source: clone C23H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTGSTIAPTTDYRNTTATGLT-----SALNLPOVHAFVNDWASLDM---WWFSIALMFV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein B01G6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T19416; T20408
R;Wilkinson, J.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19121
C;Date: 07-Apr-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 INLPOVHAFVNDW-ASLDMWWF----SIALMFVCLIIMWLICCLKRRAR 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
12.2%; Score 67; DB 2; Length 522;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 17; Conservative 9; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, February 1996 A;Reference number: 219270 A;Accession: T20408 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.1%
Matches 22, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-533 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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S52920
disintegrin (EC 3.4.24.-) - human (fragment)
Cispecies Homo sapiens (man)
Cispecies Homo sapiens (man)
Cipaces Homo sapiens (man)
Cipace (m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: PC4265
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-247 - AMCKS
A; Cross-reference: UNIPARC:UPI000017C0E0
A; Experimental source: articular chondrocyte
C; Comment: This protein is a membrane bound protein and involved in cell/cell and cell/π
C; Comment: This protein is a membrane bound protein and involved in cell/cell and cell/π
F; 126-136/Domain: metal-binding #status predicted <MEB>
F; 129-289/Domain: disintegrin homology <DIS>
                                                                                                                    A;Accession: T19413
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule: 1-1187 eWIL>
A;Cross-references: UNIPROT: Q93254; UNIPARC: UP1000017B7AA; EMBL: Z78416; PIDN: CAB01680.1;
A;Experimental source: clone C23H4
C;Genetics:
A;Genetics:
A;Geneti
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R;McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell, Biochem. Blophys. Res. Commun. 230, 335-339, 1997
A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM A;Reference number: PC4263; MUID:97168971; PMID:9016778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGSTI ----APTTDYRN-----TTATG----LTSALNLPQVHAFVNDWASLDMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 STIAP--TTDYRNTTATGLTSALNLPQV-----HAFVNDWASLDMWWFSIALMFVCLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.3%; Score 67.5; DB 2; Length 1187; Best Local Similarity 22.4%; Pred. No. 31; Matches 19; Conservative 15; Mismatches 34; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.2%; Score 67; DB 2; Length 491; Best Local Similarity 23.5%; Pred. No. 14; Matches 27; Conservative 17; Mismatches 27; Indels
                      submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WFSIALMFVCLIIMWL----IC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 IMWLICCLKRRR-----ARPPI 71
                                                                       A; Reference number: 219121
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RESULT 15
T48284

Typothetical protein T22P11.220 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C; Accession: T48284
C; Access
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12.1%; Score 66.5; DB 2; Length 428;
Best Local Similarity 25.0%; Pred. No. 14;
Matches 15; Conservative 11; Mismatches 21; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 5
A; Note: T22P11.220
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	Compugen Ltd.	
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GenCore version 5.1.6	- 2006	
GenCore	(c) 1993	
	Copyright	

January 20, 2006, 19:01:31; Search time 3753 Seconds (without alignments) 3827.241 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

1 gatgaccggctcaaccatcg.....ttcttttacagtatgattaa 307 US-10-822-873-10 307 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

41078325 segs, 23393541228 residues Searched:

82156650 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

gb_est1:*
gb_est2:*
gb_htc:*
gb_est4:*
gb_est6:*
gb_est7:*
gb_gs82:*
gb_gs83:* EST:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	CD364758 UI-H-FT2-		BF272879 GA ED001	DT112306 JGI ANNO1	AW187495 BNLGHi587	CO122313 GR Eb030	CO116311 GR Eb018		O		CG401905 ZMMBBb024	CC401331 PUHFL42TD	CG882662 ZMMBBb049	BX214284 Danio rer	CZ959245 304628 To	CV949172 PVrpvb 13	CV959926 PXrpxc 81	CL990781 ZMMBHF000	P AL497488 T. brucei	BH767271 BMBAC347H	BX757054 BX757054	CV951066 PVrpvb_47
or two and or	Ω	CD364758	BU777756	BF272879	DT112306	AW187495	CO122313	C0116311	AG974323	CV926006	BZ997163	CG401905	CC401331	CG882662	BX214284	CZ959245	CV949172	CV959926	CL990781	TA303D04P	BH767271	BX757054	CV951066
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di	Query Match	63.8	13.2	13.0	12.6	12.5	12.5	12.5	12.4	12.2	12.0	12.0	12.0	12.0	11.9	11.9	11.8	11.8	11.8	11.7	11.7	11.7	11.6
	Score	196	40.6	40	38.8	38.4	38.4	38.4	38.2	37.6	36.8	36.8	36.8	36.8	36.4	36.4	36.2	36.2	36.2	36	36	35.8	35.6
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CW336158 104 835 1 CW296187 104 777 1 CW427119 febb001f1 BX155641 Danio rer CV907775 PDrpcd 27 CD845789 DHOABOOG 2 AL573060 tr69a09.x BZ899030 CH2940 158 CX602294 CT02032A2 BH261969 CH230-177 BK140275 Danio rer CF446046 EST682391	CL279542 Ggal 93d B2193754 CH230~269 BH733089 BOMBP75TR CE614912 tigr-gss- CV906572 PDrpcd 14 BX269320 BX269320 AG536301 Mus muscu CX160091 FGAS04163 CF685536 CCACU16TR AA051869 CN0055-5
CW336158 CW296187 CW427119 BX155641 CV90775 CD845789 CD845789 CD845789 CX602294 BH261969 BH261969 BH275362 CK446046	CL279542 BZ193754 BH733089 CE614912 CV906572 EXZ69320 AG536301 CK160091 CF685536
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ALIGNMENTS

	E	¥	http://ge Seg prime POLYA=res rce	//note="Torgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: BcoR I; Site 2: Not I;
RESULT 1 CD564758/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	CKGANISM REFERENCE AUTHORS TITLE	JOURNAL	FEATURES	

NCI_CGAP_FT2'is a subtracted cDNA library_constructed from a pool of 81 RNA samples from Alveolar Macrophages from Alveolar Macrophages while different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage)

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                       the conditions, other donor macrophages in different conditions, other donor macrophages in different conditions, other donor macrophages in different construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella aureus moi 10, 24 hours; Klebsiella aureus moi 10, 3 hours; Klebsiella aureus moi 10, 34 hours; Klebsiella aureus moi 10, 34 hours; Klebsiella aureus moi 10, 34 hours; Adenoviral vector (AdS CMV eGFP), moi 500, 34 hours; Adenoviral vector (AdS CMV eGFP), moi 500, 3 hours; wt adenovirus moi 500, 24 hours; wt adenovirus will solv 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 4 hours; wt ade
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Schistosoma japonicum
Schistosoma japonicum
Schistosoma japonicum
Sukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosoma.

1 (bases 1 to 390)
Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R., Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,X.J., Wang,Z.J., Chen,Z. and Han,Z.G.
Evolutionary and blomedical implications of a Schistosoma japonicum
Complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 23-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCGCTACCGGACTTACATCTACCACAAATACACCCCCAAGTTTCTGCCTTTGTCAATA 248
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Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
some normal donor macrophages were cultured in some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATTGTGCTCAACCCACACAATGAAAATTCATAGATTGGACGGTCTGAAAC-CATGT
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SJEDNF08 SJE Schistosoma japonicum cDNA, mRNA sequence.
BU777756
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86.4%; Pred. No. 1.2e-50;
iive 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Iowa.
TAG IISSUE-Human Lung Alveolar Macrophage
TAG_LIB-UL-H-FT2
TAG_SEQ-GGGCCATGCCG"
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GA Eb0016C17f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum CDNA clone GA Eb0016C17f, mRNA sequence.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

I (bases I to 533)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11203949.
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                      192
                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 riggrijakicacigiarijaaaricakirigacaarjaakiriakirigrijikirakirik 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 CAGACGCCCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCCACAATGAAAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 grcaaaacacadaarcacrcagrrarcraargagarcarrcrcgggaaraarrcagacaa 208
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/clone="GA_Eb0016C17f"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_l: EcoRI; Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                                                                                      133 TICCAIAGCGCTTATGTTTGCCTTATTATTATGTGCGCTTATTTGTTGCCTAAAGCG
                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                                                                                                                                      DB 5, Length 390;
                                                                                                                                                                                                                                                                                                                                                        Indels
Email: hanzg@chgc.sh.cn.
Location/Qualifiers
1. 390
/organism="Schistosoma japonicum"
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/tissue_type="MRNA"
/dev_stage="egg"
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/clone_lib="SUE"
                                                                                                                                                                                                                                                                                                                                                162
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/organism="Gossypium arboreum"
/mol type="mRNA"
/strin="AKA"
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                      Query Match 13.2%; Score 40.6; DB Best Local Similarity 52.7%; Pred. No. 0.18; Matches 88; Conservative 0; Mismatches
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Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 522.
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selected using 1% agarose gel electrophoresis. (L ~0.5-1.2k, M ~1.2-5k, H ~2.5k) and then inserted into the vector using site specific recombination (flanking attB sites on cDNA). The work was done at DOB Joint Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW187495 ST 30-NOV-1999 BNLGHiS871 Six-day Cotton fiber Gossypium hirsutum cDNA 5', mRNA
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 573)
Blewitt,M., Matz,E.C. and Burr,B.
BSTS from developing cotton fiber (1999b)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 AATTGCTGGAATGTTCCATATGCGATCCACGAGTTCGGAGTTCAGCCTGGACTCCCCCACTTA 482
                                                                                                                                                                                                                                                                        98 GTCAATGACTGGGCGAGCTTGGACATGTGGTGGTTTTTCCATAGCGCTTATGTTTGC
                                                                                                                                                                                                                                                                                                                      97 IGTCAATGACTGGGCGAGCTTGGACATGTGGGTTTTTCCATAGCGCTTATGTTTG
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/tissue_type="immature fiber"

/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/clone_lib="Six-day Cotton fiber"
/note="Vector: pBluescript II KS+"
                                                                                                                                                                                                                     32;
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12.5%; Score 38.4; DB 1;
Best Local Similarity 55.1%; Pred. No. 0.95;
Matches 75; Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultivar="Acala Maxxa"
                                                                                                                                                                        Score 38.8; DB Pred. No. 0.73; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      158 CTTATTATTATGTGGCTTATTTGTTGCCTA 187
                                                                                                                                                                                                                                                                                                                                                                                                  98 CITALTALATAGLACTGLTITIGLTAATA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gossypium hirsutum (upland cotton)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burræbniuxl.bnl.gov
Seq primer: 73 Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWI87495
AWI87495.1 GI:6461931
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                                                                                                                                                                        Query Match
Best Local Similarity 64.4%;
Matches 58; Conservative
                                                                                                     Institute."
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AW187495
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/dav stage="Adult"
/clone_lib="Adult"
/clone_lib="Adult"
/clone_lib="ANNO Pimephales promelas Whole (M)"
/note="Vector: pDONR222; The library was made from dT
/note="Vector: pDONR222; The library was made from dT
primed cDNA and cloned into Invitrogen vector pDONR222.
Polly A RNA were primed with a Biotin-attB2-Oligo(dT)
primer (5' - GGCGCCCACAACTTTGTACAACAAAAAGTTGGGTT(1)19 -3')
and the first strand synthesized using Superscript II
(Invitrogen). The second strand was synthesized and an attB1 adaptor was ligated to the 5' end (5'-
TCGTCGGGGACAAAAAAAAAGTTGG -3' and 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0GI_ANNO1937.rev ANNO Pimephales promelas Whole (M) Pimephales promelas cDNA clone ANNO1937 3', mRNA sequence.
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CDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.rev'
indicates a reverse sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Poly-A: Based upon the presence of a run of 14 or more T residues
at the beginning of the sequence, this clone was polyadenylated.
The resulting Poly-T sequence has been removed.
                                                                                                                                                                                                 216
                                                                                                                                            TTTCTATTAAGAGGCTGGCTTTAACAGGTGAAGCCAGTGAAGAGTGTTTGCCATTTGTGGG 141
                                                                                                                                                                                                                                            142 AATTGCTGGAATGTTCCATATGCGATCCACGAGTCGGAGTTCAGCCTGAACCCCCACTTA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pimephales promelas
Pimephales promelas
Bukaryota, Metazota, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Pimephales.
                                                                                                                                                                                              157 CCTTATTATTATGTGGCTTATTTGTTGCCTAAAGCGCAGACGCGCCAGACCCCCCATCTA
                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 648)
Stofbardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, B.A.
DOB Joint Genome Institute Pimephales promelas EST project
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  DB 2; Length 533;
                                                  60; Indels
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Fax: 925 296 5710
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|mol type="mRNA"
|db xref="taxon:90988"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2005)
Other ESTs: JGI ANNO1937.fwd
Contact: Lindqulst,E.A., Richardson,P.
  Score 40; DB 2;
Pred. No. 0.29;
                                                  0; Mismatches
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  13.0%;
55.9%;
                                                  76; Conservative
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Query Match
Best Local Similarity
Matches 76; Conserv
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DEFINITION
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DT112306/c
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Gaps

156

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/db_xref="taxon:29730"
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/lab_host="RGR_EB"
/lab_host="Taxon: pGNV.SPORT-6.1; Site 1: Not1; Site 2:
Rooky, Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into Not1-RV. Colonies
plated/picked by AGI. More glycerol clones held in -80."
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Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Teurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 01-FEB-2005
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium. I (bases I to 865)
Kim, H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Toshio,T.K. and Sakaki,Y.
BAC end sequences of Library DNB1
Unpublished
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                                                                                                                              Global assembly of Cotton ESTs
Unpublished (2004)
Unpublished (2004)
Contact: Ming
Arizona Genomics Institute
The University of Arizona
The University of Arizona
The University of Arizona
The Sol 626 9595
Fax: 520 626 1259
Email: rwing@genome.arizona.edu
Plate: 018 row: I column: 06.
Location/Qualifiers
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/organism="Gossypium raimondii"
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GSS.
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                                                                                                                   Wing, R.A.
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/mol_txpe="mRNA"
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RocRV; Library made by Invitrogen with RNA supplied by Rendle lab. Directional cloned into Not1.EV. Colonies plated/picked by AGI. More glycerol clones held in -80."
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                                                                             GR ED03001.f GR_ED GOSSYPium raimondii cDNA clone GR_ED03001 5',
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GOSSYPJUM raimondii
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Malvales, Malvaceae; Malvoideae, Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 rrrcrarraggaggergecriraacaggigaagccagrgaagagrgrrigecarrigigg 429
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Gossypium raimondii
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                          1 (bases 1 to 856)
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Wdall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and Wing, R.A.
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwingeenome arizona.edu
Plate: 03 row: O column: 01.
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Pred. No. 1;
0; Mismatches 61; Indels (
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CO116311.1 GI:48814998
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55.1%;
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Best Local Similarity
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                                                   RESULT 6
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754 bp DNA linear GSS 25-MAR-2003 PUGFJIITD ZM 0.6_1.0 KB Zea mays genomic clone ZMMBTa371B22, genomic survey sequence.
BZ997163.1 GI:29240580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    479 ritritutiaardaddaddadcardrictccacardriatarcccarratrcrrcca 420
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1 (bases 1 to 754)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 TGTGGTGGTTTTTCCATAGCGCTTATGTTTGCCTTATTATTATGTGGCTTATTTGTT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4577"
/clone="zMMBTa37H22"
/clone_lib="zM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                   118 GGACATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTTGCCTTATTATTATGTGGCTTAT
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                     12.2%; Score 37.6; DB 8; Length 598; 54.3%; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                      64; Indels
                         1. .598
/organism="Phytophthora infestans"
/mol_type="mRNA"
/mol_type="mRNA"
/db_krain="88069"
/db_krefe="taxon:4787"
                                                                                                                                                                /clone_lib="sporangia, purified"
/note="Vector: pSPORT1"
                                                                                                                                                                                                                                                                                               0; Mismatches
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/mol_type="genomic DNA"
/strain="B73"
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Class: sheared ends.
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Other GSSs: PUGFJIITB
Contact: Cathy Whitelaw
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Best Local Similarity 50.0%
Matches 92; Conservative
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Best Local Similarity 54.3
Matches 76; Conservative
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1 (bases I to 598)

Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
Lam,S.T. and Judelson, H.S.
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(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the BAC library DSM1
For BAC library availability, please contact Masa-Toshi Yamamoto
(yamamoto@kit.jp)
Submitted (30-11-2004) by Masahira Hattori,
RIKEN, Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp,Tel:81-45-503-9111,
This work was done in collaboration with Yamamoto, M-T. Drosophila
Genetic Resource Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 ATAGGCCTATCATTGTGCTCAACCCACAATGAAAAATTCATAGATTGGACGGTCTGA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 ACGCCCTGTCACTATGCTCAGCTTACACACTGAGAAAAATACTAACTTAGAAGTCATGA 507
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Phytophthora infestans
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/organism="Drosophila simulans"
/mol_type="genomic DNA"
/mol_type="taxon:7240"
/clone="DSM1-015001.F.fa"
/clone_lib="DSM1 Drosophila BAC library"
                                                                                                                                                                                                                                                                              Saga Ippongi-cho, Ukyo-ku, Kyoto 616-8354, Japan
Tel: 81-75-873-2660 FAX: 81-75-861-0881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 12.4%; Score 38.2; DB 10;
1 Similarity 63.7%; Pred. No. 1.1;
58; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 AACCATGTTCTTTTTACAGTATGATTA 306
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University of California
Webber Hall, Riverside, CA 92521, 1
Tel: 909 787 4199
Fax: 909 787 4294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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: Sacl
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R.Site 1
R.Site 2
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Best Local Similarity
Matches 58; Conserva
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882 bp DNA linear GSS 19-MAY-2003
PUHFI42TD ZM_0.6 1.0 KB Zea mays genomic clone ZMMBTa439G12,
CC401111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (baess 1 to 882)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Besnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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/db.xref="taxon:4577"
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/clone="Lb="ZM_0-61.0 KB"
/note="Vector: pCR4-TOFO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
                            183 GAAAATATAGCATAACAATAGTTCGAAGAGGTAAACTGAATTTTCTACTTTTATATTCTC
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12.0%; Score 36.8; DB 9; Length 882;
Best Local Similarity 50.0%; Pred. No. 3.3;
Matches 92; Conservative 0; Mismatches 92; Indels
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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/strain="B73"
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/organism="Zea mays"
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Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Other GSSs: PUHFL42TB
Contact: Cathy Whitelaw
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CC401331.1 GI:30881421
GSS.
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Zea mays
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ZMMBBb0243J34.£ ZMMBBb Zea mays genomic clone ZMMBBb0243J24 5',
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1 (bases 1 to 802)
Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
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                                                                                                  521 cerccaartratratragadactrocaaccaacaccivatratratraccaaraaa 462
                                                                                                                                         243 ACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTATG 302
                                                                                                                                                                             461 GAAAATATAGCATAACAATAGTTCGAAGAGGTAAACTGAATTTTTCTACTTTTATATTCTC 402
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/loine lib==ZNMBBB
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HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing of the maize genome Unpublished (2003)
Contact: Rood Wing Arizona Institute
Miversity of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 802;
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Pred. No. 3.2;
0; Mismatches 92;
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/cultivar="B73"
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Tel: 520 626 3967
Fax: 520 621 9288
Emall: rwing@genome.arizona.edu
PCR PRimers
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Seg primer: T7
Class: BAC ends.
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1. .802
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CG401905.1 GI:34400789
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Best Local Similarity 50.0
Matches 92; Conservative
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CG401905
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Lycopersicon esculentum (Solanum lycopersicum)

Lycopersicon esculentum

Bukaryorat, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Bukaryorat, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

El (bases 1 to 991)

Mueller, L.A., Buells, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J., Van Eck, J. and Stack, S.

BAC end sequencing from three Solanum lycopersicon libraries Unpublished (2005)

Contact: Lukas Mueller

Tanksley Lab, Dept. of Plant Breeding

Cornell University

Tal: 607-255-6683

Emarson Hall, Ithaca, NY 14853, USA

Fax: 607-255-6683

Email: sgn-feedback@sgn.cornell.edu
  Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 258B20. 258B20 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 11-AUG-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304628 Tomato EcoRI BAC Library Lycopersicon esculentum genomic clone SL EcoR10001113 3, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.9%; Score 36.4; DB 10;
Best Local Similarity 52.7%; Pred. No. 4.3;
Matches 79; Conservative 0; Mismatches 71;
                                                                                                                                                               http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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/lab_host="E. coli"
                                                                                                                                                                                                                                      /organism="Danio rerio"
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High quality sequence stop: 694.
Location/Qualifiers
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Class: BAC ends
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1 (bases 1 to 956)
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Scovetz, Y., Ruks, G., Yu, Y., Wing, R. and Messing, J.
Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                        Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 768)
Humphray,S.J., Huckle, E. and Durham,J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab host="E. coli DH10B"
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Danio rerio genomic clone DKEY-258E20, genomic survey sequence
BX214284
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ZMMBBb0492E18f ZMMBBb (HindIII) Zea mays genomic clone ZMMBBb0492E18 5', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          190 Freilinghuygen Road, Piscataway, NJ 08854, USA Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
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/cultivar="B73"
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Location/Qualifiers
1. .956
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CG882662.1 GI:38613671
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                                                                                                                                                                                                                                                                                                                                                Contact: Bharti, A.K.
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Best Local Similarity
Matches 92; Conserva
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/clone_lib="Tomato EcoRI BAC Library"
/note="Vector: unk; Site_l: EcoRI"
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ORIGIN	NI / MOLGET VECTOR: MIK! SILCE_1: BOOK!	
Query	Query Match 11.9%; Score 36.4; DB 10; Length 991;	
Best Match	Best Local Similarity 55.6%; Fred. No. 4.5; Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps	°;
È	142 GCTTATGTTTGCTTATTATTATGTGGCTTATTTGTTGCCTAAAGCGCAGACGCGC 201	2 201
QQ	406 GTTTTGTAGGTTTGCAGGTTTAATATCATGCATATTATTTTGATCTATCGTTCAAGGGG 347	3 347
È	202 CAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCCACAATGAAAAAATTCATAG 261	3 261
q	346 TGADAACTCCATTCATCAACTCTTGTTATGATCAATCATCACGGGGGGAAAAATATAA 287	A 287
È	262 ATTGGA 267	
q	286 TTTGTA 281	

Search completed: January 20, 2006, 21:07:43 Job time : 3759 secs

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Mastadenovirus.
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07-DEC-1998
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                                                                                                       ; Search time 77 Seconds (without alignments) 576.328 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                             2443163 segs, 439378781 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Ad2 encod Adenoviru ADP amino Adenoviru Adenoviru Adenoviru Adenoviru Amino aci Ad6 encod Ad2 ADP m ADP m ADP m ADP m ADP C ADP P encod Adenoviru Adenoviru Amino aci Human ADP encod Aab61867 A Aab61876 A Aab61873 A Aab61869 Aab61871 Aab61865 Aab47591 Abg69353 Abu10308 Adi36347 Adv20979 Adw47775 Aaw59925 Adw28321 Aab61868 Aab61870 Aaw98003 Aab61872 AAB47591 ABG69353 ABU10308 AAB61868 AAB61870 AAB61867 AAB61876 AAB61873 AAB61866 AAM50206 ADW47775 AAW59925 ADI36347 ADV20979 AAB61872 1000.0 10 0.001 545 459 459 422 395 395 233 209

Aab61874 Ad2 ADP t	Adz13436 Human can	Add45030 Rat Prote	Abo63032 Klebsiell	Abm83572 Human dia	Abm83571 Human dia	Adg66329 Novel hum	Adz13434 Human can	Abu60695 Human mat	Aay79207 Membrane-		Solubl	Abm82908 Human dia	Abm82910 Human dia	Human	Human	Abm82912 Human dia	Aaw05809 Human tum	Aaw12659 Human her	Aaw60045 Human TNF	Aaw69238 Herpesvir
AAB61874	ADZ13436	ADD45030	AB063032	ABM83572	ABM83571	ADQ66329	ADZ13434	ABU60695	AAY79207	ABU60694	ADF50686	ABM82908	ABM82910	ABM82909	ABM82911	ABM82912	AAW05809	AAW12659	AAW60045	AAW69238
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19	172	544	521	1248	1274	199	199	239	277	277	277	282	282	282	282	282	283	283	283	283
19.8	13.8	13.4	13.3	13.1	13.1	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9	12.9
109	92	74	73.5	72	72	71	71	71	71	71	71	71	71	71	71	71	7.1	71	71	11
25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

in the B3 or B4 region. Inclusion of such a coding sequence in an adenoviral vector significantly enhances the extent of cytotoxicity, cell killing and virus production. The invention provides replication-competent adenovirus vectors which preferentially replicate in cells that express alpha-fetoprotein (AFP), particularly hepatoma cells. The vectors This is the amino acid of the adenovirus death protein (ADP) of of adenovirus type 2. The ADP coding sequence (see AAV47675), with or without the Y leader, can be introduced into an adenoviral genome, e.g. New adenovirus vector, for treating cancers - comprising an adenovirus gene under the transcriptional control of an alpha fetoprotein Adenovirus death protein; ADP; vector; hepatoma; cancer; alpha-fetoprotein transcription regulatory element; AFP-TRE; hepatocellular carcinoma; hepatoma; gene therapy; human. Schuur ER; Little AS, Lamparski HG, Henderson DR, AAW61197 standard; protein; 101 AA. Claim 29; Page 74; 102pp; English transcription regulatory element 98WO-US004084 97US-0039597P 98US-00033428 (revised)
(first entry) Adenovirus death protein. WPI; 1998-495861/42. N-PSDB; AAV47675. CALY-) CALYDON INC

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comprise at least one adenovirus gene, preferably a gene that contributes to cytotoxicity, under the transcriptional control of an AFP transcription regulatory element (see AAV47654-55). The vectors are useful for conferring selective cytotoxicity to AFP-expressing cells, especially cancer cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New adenovirus vectors, particularly for cancer therapy - comprising adenovirus gene under transcriptional control of carcinoembryonic antigen
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                                                                                                                                                                                                                                                                                                                                                              Carcinoembryonic antigen; transcriptional regulatory element; CEA-TRE; human; promoter; enhancer; vector; cancer; gene therapy; PCR; primer; adenovirus death protein; ADP.
                                                                                                                                                       MIGSTIAPTIDYRNITATGLISALNLPQVHAFVNDWASLDWWWFSIALMFVCLIIMWLIC
                                                                                                                                         MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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100.0%; Pred. No. 2.5e-61;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      AAW78902 standard; protein; 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcriptional regulatory element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US004133
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                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                   Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                         Adenovirus death protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-495862/42.
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                                                                                                        Local Similarity
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                                                                      Sequence 101 AA;
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This is the amino acid sequence of adenovirus death protein (ADP). Claimed replication-competent adenovirus (Ad) vectors comprise an Ad gene under transcriptional control of a probasin transcriptional response element (PB-TRE, see AAV57334). The vector can be used for detecting cells that allow a PB-TRE to function, especially cells expressing an androgen receptor, such as prostate cells. They can be used to confer selective toxicity to such cells. In particular, the vectors con be used for treating cancers such as prostate cells. They can be used to confer ADP gene (see AAV57354) may render the vector more potent, making possible more effective treatment and/or a lower dosage requirement. An Ad vector has been constructed that contains the ADP gene under control of PB-TRE. Cytotoxicity was demonstrated toward LNCaP (prostate
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                                     1 MIGSTIAPITDYRNITATGLISALNLPQVHAFVNDWASLDMWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New adenovirus vectors, particularly for cancer therapy - comprising an adenovirus gene under transcriptional control of a probasin transcriptional regulatory element.
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   MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probasin transcriptional response element; PB-TRE; rat; androgen receptor; adenovirus; vector; prostate cancer; gene therapy; adenovirus death protein; ADP.
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                                                                                                                              61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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100.0%; Pred. No. 2.5e-61;
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                                                                                                                                                                                                                                                                                                                                                                  AAW75787 standard; protein; 101 AA
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Matches 101; Conservative
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25-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         This protein comprises the adenovirus death protein (ADP) of adenovirus serotype 2. The invention provides novel adenovirus vectors in which at least one adenovirus gene, preferably one that contributes to cytocoxicity, is placed under transcriptional control of a human glandular kallikrein hKLK2 enhancer transcriptional regulatory element (hKLK2-TRE, see AAX24755). Such vectors are useful for treatment of cancers auch as prostate cancer. The ADP gene may render the adenoviral vector more potent, making possible more effective treatment and/or lower dosage requirement. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                     Enhancer; glandular kallikrein-1; hGK-1; hKLK2; human; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       providing increased expression of heterologous sequences in prostatic cells, and related adenoviral vectors for treating prostatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 551; DB 2; Length 101; 100.0%; Pred. No. 2.5e-61; ive 0; Mismatches 0; Indels
CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 165-166; 179pp; English.
                                                            AAW98003 standard; protein; 101 AA
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                                                                                                                                                               therapy; adenovirus death protein.
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98US-0076545P.
98US-00127834.
                                                                                                                                                                                                                                                98WO-US016312,
                                                                                                              (first entry)
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                                                                                                                                  Adenovirus death protein.
                                                                                                                                                                                   Human adenovirus type 2.
                                                                                                    (revised)
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                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-153804/13.
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21-JUN-1999
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AAY84407
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The present sequence represents an adenoviral death protein, which is used to construct the vectors of the invention. The specification describes adenoviral vectors which comprise an adenovirus gene under transcriptional control of a cell status specific transcriptional regulatory element (TRE). The TRE is preferably one that is essential for adenovirus vectors may be used for the treatment of a range of tumours such as lung, stomach, breast, colon and rectum, and uterine and cervix cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
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                                                             adenoviral vector; adenovirus gene; transcriptional control;
transcriptional regulatory element; TRB; adenoviral propagation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLKRRRARPPIYRPIIVINDHNEKIHRLDGLKPCSLLLQYD 101
Amino acid sequence of an adenoviral death protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ad2 encoded adenovirus death protein (ADP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 9; 79pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB61866 standard; protein; 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 101; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0099791P.
                                                                                                                                                                                                                                                                                                                                                                                            99WO-US020718
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                                                                                                                             death protein; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henderson DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-271456/23.
N-PSDB; AAZ99937.
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The invention relates to a recombinant vector (V1) which is replication-
competent in a neoplastic cell and which overexpresses an adenovirus
death protein (ADP). The vector can be used in a method for promoting
death of a neoplastic cell that comprises contacting the neoplastic cell
in the least one V1; and a composition comprising V1 and a second
recombination virus which is: (a) replication defective and which
expresses an anti-cancer gene product, where V1 complements replication
of the second recombinant virus; or (b) replication-competent in a
neoplastic cell. V1, together with one or more replication-defective
adenovirus which expresses an anti-cancer gene product, are useful in
cancer therapy. Overexpression of ADP by V1 results in faster lysis of
cells and spread of the virus throughout a cell monolayer than viruses
expressing wild-type levels of ADP. The present sequence represents the
amino acid sequence of an ADP encoded by Ad2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant vector which is replication-competent in a neoplastic cell and overexpresses an adenovirus death protein, useful in cancer therapy when used together with replication-defective adenovirus which expresses
                                                                        /note= "transmembrane domain (AAB61874); fragment specifically claimed for"
                                                                                                                                               63. 70 / AAB61875)
'note= "putative lumenal domain (AAB61873)"
                                    "fragment specifically claimed for"

    101
    note= "cytoplasmic-nucleoplasmic domain"

                                                                                                                                                                                   fragment specifically claimed for"
                                                                                                                                                                                                                                                                                                                                                                                                        Tollefson AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 156; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Toth K, Doronin K,
                                                                                                                                                                                                                                                                                               12-JUL-2000; 2000WO-US018971.
                                                     .59
                                                                                                                                                                                                                                                                                                                                                                     (UYSL-) UNIV SAINT LOUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an anti-cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-103079/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 101 AA;
                                                                                                                                                                                                                        WO200104282-A2
                                                                                                                                                                                                                                                            18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                          Wold WSM,
                   Peptide
                                                                                                               Domain
                                                       Domain
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                                                                          1 MIGSTIAPTIDYRNTTATGLISALNIPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                          MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                 Gaps
                                ö
Length 101;
                              0; Indels
                                                                                                                                    CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLLQYD 101
                                                                                                                     CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
 100.0%; Score 551; DB 4;
100.0%; Pred. No. 2.5e-61;
tive 0; Mismatches 0;
                              101; Conservative
   Query Match
Best Local Similarity
                                                                                                                                                 61
                                Matches
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ADP amino acid sequence.
                                                                                                                                      unidentified adenovirus
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AAM50206 standard; protein; 101 AA

(revised)
(first entry)

07-JAN-2002 11-SEP-2003

AAM50206;

AAM50206
ID AAM5
XX
AC AAM5
XX
DT 11-5
DT 07-2
XX
DE Ader

Adenovirus death protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of the adenovirus death protein (ADP). The ADP gene coding region (see AAI70186) was obtained by PCR amplification and used in the construction of adenoviral vectors in which ADP expression was under the control of a urothelial cell-specific transcriptional regulatory element (TRE) derived from the human uroplakin II gene 5' flanking region (see AAI70144). This is an example of preferably an adenovirus gene, under transcriptional control of a urothelial cell-specific TRE. They display urothelial cell-specific cytotoxicity, and are used for the specific, targeted gene therapy of bladder cancer. (Updated on 11-SEP-2003 to standardise OS field)
            Adenovirus death protein; uroplakin II; vector;
transcriptional regulatory element; TRE; urothelial cell; bladder cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                  Human urothelial cell specific uroplakin transcriptional regulatory sequences, useful for producing adenoviral vectors which can be used to confer selective cytotoxicity to target cells, especially bladder cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenovirus, ADP; replication-competent, adenoviral vector; TRE; transcriptional regulatory element; mutation, deletion, IRES; promoter; internal ribosome entry site; cytotoxic; cancer; bladder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 551; DB 4; Length 101; 100.0%; Pred. No. 2.5e-61; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB47591 standard; protein; 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Fig 12; 147pp; English.
                                                                                                                                                                                                                                                                                  Zhang H, Henderson DR;
                                                                                                                                                                                 21-MAR-2001; 2001WO-US009224.
                                                                                                                                                                                                                  24-MAR-2000; 2000US-0191861P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 101; Conservative
                                                                               Human adenovirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                               human; gene therapy.
                                                                                                                                                                                                                                                                                                                     WPI; 2001-639229/73.
                                                                                                                                                                                                                                                  (CALY-) CALYDON INC
                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAI70186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 101 AA;
                                                                                                                WO200172994-A2
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                                                                                                                                                 04-OCT-2001
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This sequence represents adenoviral ADP. The ADP coding sequence may be used in the replication-competent adenoviral vector (A) of the invention which contains two genes (G1, G2) that are co-transcribed as a single mRNA and under control of a heterologous, target cell-specific transcriptional regulatory element (TRE). G2 has a mutation in, or deletion of, its endogenous promoter and is controlled from an internal ribosome entry site (IRES). The ADP coding sequence may be used as G1 or G2. (A) has greater specificity for a target cell than a similar vector in which TRE is operably linked to a gene and which lacks an IRES. (A) are used to modify the genotype of target cells, optionally in vitro with subsequent return of altered cells to the host and where G2 is a cytotoxic gene, to confer selective cytotoxicity to target cells, especially for killing cancer cells. Oh are used for diagnosis and monitoring, e.g. detection of bladder cancer cells. The target cells, performing the minimal replication in non-target cells, so a runaway infection is prevented but production of adenoviral proteins in target cells activates cand/or stimulates the immune response against target cells producing such proteins. The use of an IRES (rather than two identical control elements) control elements) extra apace for an additional (therapeutic) gene. (Updated on 11-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIGSTIAPTIDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMMLIC 60
                                                                                                                                                                                                                                                                                                Replication-competent adenoviral vector, useful e.g. for killing cancer cells, contains two genes linked by internal ribosome entry site and controlled by target-specific regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adenovirus; transcriptional regulatory element; TRE; prostate; liver; breast cancer; colon cancer; antitumour; adenovirus death protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 551; DB 4; Length 101; 100.0%; Pred. No. 2.5e-61; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG69353 standard; protein; 101 AA
                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 9; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adenovirus death protein (ADP).
                                                                              21-MAR-2001; 2001WO-US009036.
                                                                                                                   24-MAR-2000; 2000US-0192156P.
                                                                                                                                                                                               Li Y, Henderson DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.7
Matches 101, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to standardise OS field)
                                                                                                                                                                                                                                      WPI; 2001-639234/73.
                                                                                                                                                          (CALY-) CALYDON INC
                                                                                                                                                                                                                                                          N-PSDB; AAH43535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 101 AA;
WO200173093-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-OCT-2002
                                       04-OCT-2001
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The invention relates to an adenovirus vector (AV) comprising an AV gene under transcriptional control of a cell type-specific transcriptional regulatory element (TRE) and optionally a first AV gene under control of a first cell type-specific TRE and a second gene under control of second cell type-specific TRE, where the first and second cell type-specific TREs are substantially identical. When the vector is introduced into a cell (e.g. prostate cell, liver cell, breast cancer cell or colon cancer cell) it allows the cell type-specific TRE to function, resulting in cytotoxicity. The vector is useful for suppressing tumour growth of a target cell. This sequence represents a polypeptide used in the scope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                                                      Novel adenovirus vector comprises adenovirus gene under transcriptional control of cell-type specific transcriptional response element for conferring selective toxicity on target cell and for suppressing tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenoviral vector, adenovirus gene; transcriptional control; TRE; cell type-specific; transcriptional response element; PSA; hKLK; prostate-specific antigen; glandular kallikrein; probastin; PB; carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUC1; cytotoxicity; neoplasia; tumour growth; gene therapy; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 551; DB 5; Best Local Similarity 100.0%; Pred. No. 2.5e-61; Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU10308 standard; protein; 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 19; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adenovirus death protein (ADP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenovirus death protein; ADP.
                                                                                                      06-DEC-2000; 2000US-00732169.
                                                                                                                                         98US-00151376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                Schuur ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified adenovirus
                                                                                                                                                                          (HEND/) HENDERSON D
(SCHU/) SCHUUR E R.
                                                                                                                                                                                                                                                                    WPI; 2002-582468/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 101 AA;
                                                                                                                                                                                                                                                                                    N-PSDB; ABK99587
                                 US2002068049-A1
                                                                                                                                                                                                                              Henderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the invention
Unidentified.
                                                                                                                                         10-SEP-1998;
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07-AUG-2003
                                                                    36-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                              growth.
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US2003044383-A1

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US2003152553-A1.
Homo sapiens.
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SXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                             adenovirus gene under transcriptional control of a cell type-specific transcriptional response element (TRE). Example TRES given in the specification include human prostate-specific antigen (FSE) TRE, human glandilar kallikrein (HKLK) TRE, rat probastin (FSE) TRE, human carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3 (WICL) TRE. The modified adenovirus vector is useful as a vehicle for introducing new genetic capability, particularly associated with cytotoxicity for treating neoplasia. For example, the vector may be used in a target cell to suppress tumour growth, or to kill the target cell. The vector is particularly useful in gene therapy. The present sequence represents adenovirus death protein (ADP). (Updated on 23-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MIGSTIAPITDYRNTTATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                             New adenovirus vector for transfecting target host cells, comprises ar adenovirus gene under transcriptional control of a cell type-specific transcriptional response element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; prostate; transcriptional response element; TRE; polyethylene glycol; PEG; masking agent; tumour cell growth; proliferation; psoriatic lesion; wound healing; hyperplasia; cancer; cytostatic; antipsoriatic; vulnerary; ADP.
                                                                                                                                                                                                                                                                                                                                                      The present invention relates to adenoviral vectors comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 100.0%; Score 551; DB 6; Length 101; Best Local Similarity 100.0%; Pred. No. 2.5e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ADP protein sequence SeqID 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI36347 standard; protein; 101 AA.
                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 19; 83pp; English
                                                       95US-00495034.
96US-00699753.
97US-0039597P.
97US-0039599P.
97US-0039762P.
                                                                                                                                 98US-00033333
98US-00033428
                                  98US-00151376
                                                                                                                                                         98US-00033555
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                                                                                                                                                                                                                    Henderson DR, Schuur ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 101; Conservative
                                                                                                                                                                                  HENDERSON D R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standardise OS field)
                                                                                                                                                                                                                                          WPI; 2003-456547/43.
N-PSDB; ACD07312.
                                                                                                                                                                                            SCHUUR E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 101 AA;
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                                                                               03-MAR-1997;
03-MAR-1997;
03-MAR-1997;
03-MAR-1997;
                                  10-SEP-1998;
                                                                                                                                                         02-MAR-1998;
           06-MAR-2003.
                                                                                                                                 02-MAR-1998
02-MAR-1998
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                                                                                                                                                                                            (SCHIU/)
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AD136347
ID AD136
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AC AD136
XX
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DT 22-AP
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KW humar
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KW polye
KW polye
KW proli
KW cytos
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This invention relates to a novel composition that contains a replication competent adenovirus capable of transfecting target host cells. Specifically, it comprises an adenoviral gene essential for replication (ELA, ELB or E4), which is under the transcriptional control of a prostate specific transcriptional response element (TRE) and polyethylene (ELA, ELB or E4), which is under the transcriptional control of a prostate specific transcriptional response element (TRE) and polyethylene (ELA, ELB or E4), which is uppressing tumour cell growth and for lowering the levels of tumour cell survey and solvering transfant expression that may be involved in treating undesired proliferations other than tumours, such as speciatic lesions and wound healing. In addition, it is useful for detecting cells where a cell type-specific TRE is functional in a biological sample and for treating prostate-associated diseases such as hyperplasia and cancer. As such, these compositions exhibit cytostatic, antipsoriatic and vulnerary activities. This polypeptide sequence is the human ADP protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition comprising replication competent adenovirus having adenovirus gene essential for replication under transcriptional control of cell type specific transcriptional response element and masking agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTGSTIAPTIDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 11; 115pp; English
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                                                                                                                                   27-JUN-1995, 95US-00495034.

26-JUN 1996, 96US-00669753.

03-MAR-1997, 97US-0039597P.

03-MAR-1997, 97US-0039762P.

02-MAR-1998, 98US-00033333.

02-MAR-1998, 98US-00033555.

10-SEP-1998, 98US-00033555.

10-SEP-1998, 98US-00033555.
                                                                 02-MAY-2002; 2002US-00139089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LITTLE A S.
LAMPARSKI H G.
HENDERSON D R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-119002/12.
N-PSDB; ADI36417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCHU/) SCHUUR E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 101 AA;
14-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
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(LAMP/)
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Gene therapy; vector; prostate tumor; cytostatic; vasotropic; vulnerary;
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                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to an adenovirus vector comprising an adenovirus early gene essential for propagation under the control of a human prostate specific antigen promoter and a human prostate specific antigen (PGA) enhancer. The invention is useful for treating a patient suffering from prostate cancer and for making mammalian hosts that are transiently transgenic and for detecting the presence of cells that permit the function of a cell type-specific transcriptional regulatory element (TRE) in a sample. The invention is also used in the gene therapy and also as vaccine. The present sequence is the adenovirus death protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                        Vector; gene transfer; cloning vehicle; genetic engineering; prostate cancer; gene therapy; vaccine; cytostatic; prostate-specific antigen; TRE; transcriptional regulatory element; PSE; prostate specific enhancer; PSA; prostate specific enhancer; ADP.
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                                                                                                                                                                                                                                                                                                                               New adenovirus vector comprising an adenovirus early gene essential for propagation under the control of a human prostate specific antigen promoter and a human prostate specific antigen enhancer, for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCL.IMWLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MIGSTIAPITDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 551; DB 9;
100.0%; Pred. No. 2.5e-61;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 11; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADW47775 standard; protein; 101 AA
                     Adenovirus death protein (ADP).
                                                                                                                                                                                                      26-JUN-1996; 96US-00669753.
10-SEP-1998; 98US-00151376.
06-DEC-2000; 2000US-00732169.
                                                                                                                                                                        13-APR-2004; 2004US-00822873
                                                                                                                                                                                              95US-00495034
(first entry)
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                                                                                                                                                                                                                                                                                     Henderson DR, Schuur ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adenovirus death protein.
                                                                                                         unidentified adenovirus.
                                                                                                                                                                                                                                                  (HEND/) HENDERSON D R.
                                                                                                                                                                                                                                                                                                          WPI; 2005-011642/01.
                                                                                                                                                                                                                                                                SCHUUR E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 101 AA;
                                                                                                                              JS2004241857-A1
                                                                                                                                                                                             27-JUN-1995;
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ID ADW4
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AC ADW4
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OT 07-2
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The present sequence in the protein sequence of a demovitue weetor comprises an inducible transcriptional transactivator (TT) coding sequence under the transcriptional control of a cell type-specific TRE (CT-TRE); and an adanovirus gene is preferably a gene essential for adenoviral control of a crivate by the inducinal control of a second gene under transcriptional control of a second TRE, where the TT and a second gene under transcriptional control of a second gene may an adenovirus control of a second gene under transcriptional control of a second gene who inducible TT coding sequence under transcriptional control of a second gene who inducinal gene essential for adenovirus replication, or a transgene such as a cytotoxic gene. One embodiment of the invention provides adenovirus control of a second transactivator regulated TRE, where the cure ranscriptional control of a second transactivator regulated TRE, where the comprising the replication competent adenovirus vector, and methods for propagating and regulating the vector and polymore of the propagating and regulating the vector and concept of a target tumor cell line involves introducing the adenovirus causes lysis of target prostate cells. The adenovirus vector can also be repair, enhanced immune response, resistance to infection, production of a crepair, enhanced immune response, resistance of infection, production of factors, enhanced immune response, resistance of infection, production of sectors of the viral for replication of metabolic or other physiological pathways, or comparison of activity of cells in the envelopment of a viral centerial for repease of the viral center of the envelopment in th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New replication competent adenovirus vector comprising an inducible transcriptional transactivator coding sequence and an adenovirus gene, useful for treating cancer, psoriatic lesions, restenosis or wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTGSTIAPTTDYRNTTATGLISALNLPQVHAFVNDWASLDMWWFSIALMFVCLIIMWLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the protein sequence of adenovirus death
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
antipsoriatic; antimicrobial; immunomodulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 11; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                           24-FEB-2004; 2004WO-US005518
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2003; 2003US-0450232P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CELL-) CELL GENESYS INC.
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                                                                                        Human adenovirus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-102098/11.
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Novel isolated polynucleotide comprising nucleotide sequence of yeast cytosine deaminase/mutant SR 39 herpes simplex virus type 1 thymidine kinase fusion gene, useful for treating mammalian patient having malignancy or solid tumor.
                                                 chemotherapy; cytosine deaminase; thymidine kinase; death protein;
                          Amino acid sequence of adenovirus type 5 adenovirus death protein.
                                                                cancer; neoplasm; 5-fluorocytosine; ganciclovir.
                                                                                                                                                                                                                                                                                                    Barton K, Paielli D;
                                                                                                                                            /note= "Ala encoded by AAG"
                                                                                                     ,
Misc-difference 63
                                                                                                                                                                                                                                                                            (FORD-) FORD HEALTH SYSTEM HENRY
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 54; 62pp; English.
                                                                                                                                                                                                                                                09-JUL-2003; 2003US-0486219P.
                                                                                                                                                                                                                         09-JUL-2004; 2004WO-US022320
07-APR-2005 (first entry)
                                                                                           Human adenovirus type
                                                                                                                                                                                                                                                                                                      Kim JH,
                                                                                                                                                                                                                                                                                                                                WPI; 2005-101983/11
                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADW28319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 101 AA;
                                                                                                                                                                      WO2005007109-A2
                                                                                                                                                                                                                                                                                                      Freytag SD,
                                                                                                                                                                                               27-JAN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of adenovirus death protein (ADP). The invention provides replication-competent adenovirus vectors specific for target cells and methods of using such vectors. The vectors contain heterologous transcription regulatory elements (TREs) and may incorporate a gene, such as the ADP gene (see AAV53632), which can contribute to cytocoxicity in the target cell. Adenoviral replication can be restricted to target cells in which the heterologous TREs are functional and thus the vectors can provide selective cytocoxicity to the target cells (e.g. prostate, liver, breast or colon), particularly neoplastic cells
                                                                                                                                                                      Adenovirus death protein; ADP; transcription regulatory element; vector; breast cancer; prostate cancer; liver cancer; colon cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New adenovirus vectors, used for treating tumours - comprising first and second adenovirus genes under control of different heterologous transcriptional regulatory elements.
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CLKRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLOYD 101
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                                                                 AAW59925 standard; protein; 101
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                                                                                                                                              Adenovirus death protein.
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The specification describes a polynucleotide comprising a nucleotide sequence of yeast cytosine deaminase/mutant SR39 herpes simplex virus type 1 thymidine kinase fusion gene, and further comprising an adenovirus type 5 adenovirus death protein gene. The polynucleotide of the invention limits the side effects of cancer treatment by using only lower doses of radiation. The polypeptide encoded by the above polynucleotide is useful for converting 5-fluorocytosine or ganciclovir into active chemocherapeutic agents. Pharmaceutical compositions comprising recombinant adenoviruses comprising polynucleotides of the invention are useful for treating a mammalian patient having a malignancy or solid tumor. The present sequence reperseants an adenovirus type 5 adenovirus death protein, which is used to construct polynucleotides of the
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ADW28321 standard; protein; 101 AA

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generate two sets of results each. The Published_Applications databases have been split into two parts to Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published Applications Main databases. Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New). This Page Blank (uspto)

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Copyright (c) 1993 - 2006 Compugen Ltd.
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Sequence 2922, Ap Sequence 173, Appl Sequence 173, Appl Sequence 17, Appli Sequence 11, Appli Sequence 18, Appli Sequence 1812, A Sequence 38512, A Sequence 48344, A Sequence 53863, A Sequence 60307, A Sequence 30827, A Sequence 60307, A Sequence 30686, A Sequence 30686, A Sequence 30686, A
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US-10-750-185-38512

US-10-750-185-48344

US-10-750-185-38834

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| Publication No. US2006000884A1
| GENERAL INFORMATION:
| APPLICANT: Hearing, Patrick
| APPLICANT: Bahou, Wadie
| APPLICANT: Bandalon, Ziv
| APPLICANT: Bandalon, Ziv
| APPLICANT: Gratenko, Dmitri
| TITLE OF INVENTION: Adenoviral Vectors
| FILE REFERENCE: STOWED-04970
| CURRENT APPLICATION NUMBER: US/11/127,832
| CURRENT FILING DATE: 2005-05-12
| PRIOR APPLICATION NUMBER: US/09/782,378
| PRIOR APPLICATION NUMBER: 60/237,747
| PRIOR FILING DATE: 2000-10-02
| NUMBER OF SEQ ID NOS: 27
| SOOFTWARE: PatentIn Version 3.0
| SEQ ID NO 3
| LENGTH: 35937
| TYPE: DNA TYPE: DN
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ORGANISM: Artificial Sequence
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241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
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APPLICANT: Ano, Jianfeng
APPLICANT: Ano, Jianfeng
APPLICANT: Hu, Yunping
APPLICANT: Lu, Yunping
APPLICANT: Chen, Gang
APPLICANT: Gao, Ginglei
TITLE OF INVENTION: CONSTRUCT OF TUMOR-SELECTIVE RECOMBINANT
TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
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TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
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TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
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TITLE OF SECONDING FOR THE SAME
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Pred. No. 1.2e-57;
0; Mismatches 35; Indels 1
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Sequence 2, Application US/10860436

Publication No. US2050271622A1

GENERAL INFORMATION:

APPLICANT: Zhou, Jianfeng
APPLICANT: Ma, Ding

APPLICANT: Wang, Shixuan
APPLICANT: Wang, Shixuan
APPLICANT: Chen, Gang
APPLICANT: Go, Ginglei

TITLE OF INVENTION: CONSTRUCT OF TUMOR-SELECTIVE RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29514 rcirriciciracaciarcarra 29537
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                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10860436; Publication No. US20050271622A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.8%;
Best Local Similarity 86.4%;
Matches 228; Conservative
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                                                                                                                                 TGATTAA 307
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LENGTH: 35696
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                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: recombinant adenovirus delta920-946ADV5/ASPLK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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   ADENOVIRUS, METHODS FOR PREPARING THE SAME AND USES THEREOF
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63.8%; Score 196; DB 8;
Best Local Similarity 86.4%; Pred. No. 1.2e-57;
Matches 228; Conservative 0; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
63.8%; Score 196; DB 7;
Best Local Similarity 86.4%; Pred. No. 1.2e-57;
Matches 228; Conservative 0; Mismatches 35
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Subjection No. US2006000884A1
Subjection No. US2006000884A1
GENERAL INFORMATION:
APPLICANT: Bahou, Wadie
APPLICANT: Bahou, Wadie
APPLICANT: Sandalon, Ziv
APPLICANT: Sandalon, Ziv
APPLICANT: Sandalon, Ziv
APPLICANT: Sandalon, Ziv
CURRENT APPLICATION NUMBER: US/11/127,832
CURRENT APPLICATION NUMBER: US/09/782,378
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: US/09/782,378
PRIOR FILING DATE: 2001-02-12
TITLE OF INVENTION: ADENOVIRUS, METHODS FOR TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 850141.402 CURRENT APPLICATION NUMBER: US/10/860,436; CURRENT FILING DATE: 2004-06-03; NUMBER OF SEQ ID NOS: 15 SOFTWARE: FABLESEQ for Windows Version 4.0; SEQ ID NO 2: LENGTH: 35893
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                                                                                          TCATTGTGCTCAACCCACACAATGAAAAATTCATAGATTGGACGGTCTGAAAC-CATGT 283
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 Query Match 63.8%; Score 196; DB 8; Length 35935; Best Local Similarity 86.4%; Pred. No. 1.2e-57; Matches 228; Conservative 0; Mismatches 35; Indels 1
                                                                                                                                                                                                               TCTCTTCTTTACAGTATGATTAA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human adenovirus type
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 35935
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US-11-066-480-5
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Sequence 4, Application US/10857780

| Sequence 4, Application US/10857780
| Publication No. US2005027204341
| GENERAL INPORMATION:
| APPLICANT: ROTH, RICHARD B. |
| APPLICANT: BRAUN, ANDREAS |
| APPLICANT: REMELAND, RIKAND HERRY |
| APPLICANT: REMELAND, RIKAND HERRY |
| APPLICANT: REMELAND, MATTHEW ROBERTS |
| APPLICANT: REMELAND, MATTHEW ROBERTS |
| APPLICANT: HOYAL-WRIGHTSON, CAROLYN R. |
| TITLE OF INVENTION: THEREOF |
| TITLE OF INVENTION: HERRED |
| TITLE OF INVENTION: THEREOF |
| FILE REFERENCE: SEQ-4069-0F |
| CURRENT APPLICATION NUMBER: US/10/857,780 |
| PRIOR PILING DATE: 2003-07-24 |
| PRIOR FILING DATE: 2003-11-25 |
| PRIOR FILING DATE: 2003-11-25 |
| PRIOR FILING DATE: 2003-11-25 |
| SOFTWARE: Patentin version 3.2 |
| SEQ ID NO 4 |
| LENGTHARE |
| LENGTHARE: Patentin version 3.2 |
| LENGTHARE: Patentin version 3.2 |
| LENGTHARE: Patentin PUBLICAND CONTINUED CON
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47.2%; Score 145; DB 8; Length 1172;
Best Local Similarity 86.5%; Pred. No. 1.6e-40;
Matches 160; Conservative 0; Mismatches 25; Indels
TITLE OF INVENTION: ONCOLYTIC ADENOVIRAL ENCODING GM-CSF FILE REFERENCE: GTIN-001
CURRENT APPLICATION NUMBER: US/11/066,480
CURRENT FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: US/10/925,205
PRIOR FILING DATE: 2004-08-23
PRIOR FILING DATE: 2004-08-28
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NOS: 5
LENGTH: 1172
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FEATURE:
NAME/KEY: misc feature
LOCATION: (16914)..(16914)
OTHER INFORMATION: n is a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ## Publication No. US20050287570A1
| GENERAL INDORMATION:
| APPLICANT: Wpeth |
| APPLICANT: Wpeth |
| APPLICANT: Wpeth |
| APPLICANT: Wpeth |
| TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes |
| TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes |
| FILE REFERENCE: 031896-041000 (AMI01086) |
| CURRENT FILING DATE: 2005-05-25 |
| PRIOR APPLICATION NUMBER: US 60/574,294 |
| PRIOR PILING DATE: 2005-06-26 |
| NUMBER OF SEQ ID NOS: 362830 |
| SOFTWARE: PatentIn version 3.2 |
| LENGTH: 2926 |
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APPLICANT: MU GENONICS, INC.
APPLICANT: MU GENONICS, INC.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REPRENCE: MMILIOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT PILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 4960
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.8%; Score 33.2; DB 8; Length 2926; Best Local Similarity 59.6%; Pred. No. 0.31; Matches 56; Conservative 0; Mismatches 38; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 CGCTTATGTTTGCCTTATTATGTGGCTTATTTGTTGCCTAA 188
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ORGANISM: Bovine 19866881284640
                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3556
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; NAME/KEY: misc_feature
; LOCATION: (117565)..(117565)
; OTHER INFORMATION: n is a, c, g, or t
US-10-857-780-4
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                            LOCATION: (19266)..(19266)
OTHER INFORMATION: n is a, c, g,
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NAME/KEY: misc_feature
LOCATION: (61207).
OTHER INFORMATION: n is a, c,
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LOCATION: (64980)..(64980)
OTHER INFORMATION: n is a, c,
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LOCATION: (81452)..(81452)
OTHER INFORMATION: n is a, c,
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LOCATION: (103359) .(103359)
OTHER INFORMATION: n is a, c,
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NAME/KEXY: misc_feature
LOCATION: (13467)..(34472)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (57355)..(57355)
OTHER INFORMATION: n is a,
                                                                                             NAME/KEY: misc feature
LOCATION: (26334)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (38627) ..(38628)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (64987) .. (64987)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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LOCATION: (95893)..(95
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         NAME/KEY: misc feature
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Best Local Similarity
Matches 68; Conserva
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US-10-750-623-49060 ; Sequence 49060, Application US/10750623

RESULT 10

RESULT 8 US-11-136-527-3556/c ; Sequence 3556, Application US/11136527

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264 TGGACGGTCTGAAACCATGTTCTCTTTTTACAGTATG 302
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Publication No. US20050287531A1
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; ORGANISM: Bovine 19866880533767
US-10-750-623-47255
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                                                                                                                                        APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR PILING DATE: 2002-12-31
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10.2%; Score 31.2; DB 7; Length 872;
Best Local Similarity 55.6%; Pred. No. 0.85;
Matches 60; Conservative 0; Mismatches 48; Indels
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APPLICANT: HOLM, Town
APPLICANT: BAIES, Stephen
APPLICANT: PANITN
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIL100-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
WUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VETSION 3.1
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Publication No. US20050260603A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Bovine 19866881284640
US-10-750-623-49060
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; ORGANISM: Bovine 19866880533767
US-10-750-185-47255
       GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENPELD, David
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 49060
LENGTH: 872
Publication No. US20050287531A1
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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Matches 79; Conservative
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US-10-750-185-47255
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LENGTH: 1542
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 4007, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

TITLE OF INVENTION UNDERR: US/11/136,527

CURRENT APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOUTHARE: Patentin version 3.2

SEQ ID NO 4007
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                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: EDENIES, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennie
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
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10.0%; Score 30.6; DB 8; Length 1009;
Best Local Similarity 47.2%; Pred. No. 1.5;
Matches 93; Conservative 0; Mismatches 104; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.1%; Score 31; DB 7; Length 1542; Best Local Similarity 49.7%; Pred. No. 1.3; Matches 79; Conservative 0; Mismatches 80; Indels
490 ricaracriciragagrericacririririgiraagagrig 528
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CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
FRIOR APPLICATION NUMBER: US 60/437,482
FRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 47255
LENGTH: 1542
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APPLICATION NUMBER: PCT/US03/29906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 AACATCATCCCCTGGCACTGACCTAAGCAAGAATCAGGCCATGAAGGAAAAGGAGAGCT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 TICCATAGOGCITATGTITGTTTGCCTTATTATTATGTGGCCTTATTTGTTGCCTAAAGCG 192
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                                                                      176 AACATCATCCCTCGCCACTGACCTAAGCAAGAATCAGGCCATGAAGGAAAAGGAGAGGCT 235
                                                                                                                     133 TICCAIAGCGCTIAIGITIGITIGCCTIAITAITAIGIGCTTAITIGITGCCTAAAGCG 192
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                          73 AAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGACATGTGGTGGTTT 132
                                                                                                                                                                 236 GATTAAAGAGCTGCAGCTCATTACCGAGGAGAAATGACCTGAGAAGATCGCCTGAAGTT 295
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Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVERTION: Probe Arrays For Expression Profiling of Rat Genes

TITLE OF INVERTION NUMBER: US/11/136,527

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-26

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                           356 CCTGGAGAGATGGAGG 372
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Sequence 1, Application US/11091018
Publication No. US20050287551A1
GENERAL INFORMATION:
APPLICANT: Gretaredottir, Solveig
APPLICANT: Thorleifsson, Gudmar
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: METHODS OF TREATMENT
TITLE OF INVENTION: METHODS OF TREATMENT
TITLE OF INVENTION: METHODS OF TREATMENT
CURRENT APPLICATION UNMBER: US/11/091,018
CURRENT FILING DATE: 2005-03-25

US-11-091-018-1

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52 TACCGGACTAACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGC 111
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Pred. No. 73;
0; Mismatches 78; Indels 0;
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PRIOR FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 10/255,120
PRIOR FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 10/419,723
PRIOR APPLICATION NUMBER: 10/419,723
PRIOR FILING DATE: 2003-04-18
PRIOR FILING DATE: 2003-08-27
PRIOR FILING DATE: 2002-02-04
PRIOR PLING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 10/067,514
PRIOR APPLICATION NUMBER: 09/811,352
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 102
SEQ ID NO :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: January 20, 2006, 21:30:39 Job time : 397 BECB
                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(1691140)
; OTHER INFORMATION: n=A,T,C or G
US-11-091-018-1
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Best Local Similarity 49.7%;
Matches 77; Conservative
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NAME/KEY: misc_feature
LOCATION: (1)...(169114
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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Sequence 15, Appl
Sequence 3, Appli
                                                                        ; Search time 803 Seconds (without alignments) 3161.518 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Api
Sequence 731, 2
Sequence 5, Api
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Sequence 10,
Sequence 61,
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Sequence 7, A
Sequence 2, A
                                                                                                                                                    1 gatgaccggctcaaccatcg......ttcttttacagtatgattaa 307
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Sequence 17
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-392-822-8
US-09-814-292-3
US-09-814-292-3
US-09-151-376-10
US-09-151-376-10
US-09-151-376-11
US-10-84-351-17
US-10-94-11-19
US-10-139-089-10
US-10-139-089-10
US-10-139-089-10
US-10-822-873-10
US-10-822-873-10
US-10-822-873-10
US-10-822-873-10
US-10-822-873-10
US-10-822-873-10
US-10-938-277-61
US-10-938-277-61
US-10-94-514A-731
US-10-94-514A-731
US-10-785-739-15
US-10-659-739-15
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                  nucleic search, using sw model
                                                                           2006, 19:21:44
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Gapop 10.0 , Gapext 1.0
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APPLICANT: Yu, De Chao
APPLICANT: Yu, De Chao
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Adenovirus Vectors Slements and Methods of Use Thereof
FILE REFERENCE: 348022001200
CURRENT APPLICATION NUMBER: US/09/392,822
CURRENT APPLICATION NUMBER: US/09/392
EARLIER FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 307
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100.0%; Pred. No. 2.3e-91;
ive 0; Mismatches 0;
                                                         US-10-860-630-2

US-09-725-720-43

US-09-782-730-44

US-09-782-378A-4

US-10-264-839-12

US-10-432-989-11

US-10-432-989-11

US-10-492-178-9

US-10-492-178-9

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US-09-952-060-30
US-10-380-641-30
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US-09-952-060-25
US-10-380-641-25
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Patent No. US20010053352A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 307; Conservative
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TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
              FILE REFERENCE: 348022000900
CURRENT APPLICATION NUMBER: US/09/875,228
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/127,834
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: 60/076,545
PRIOR APPLICATION NUMBER: 60/054,523
PRIOR PILING DATE: 1998-03-02
PRIOR PILING DATE: 1998-03-05
NUMBER: 0F SEQ ID NOS: 38
SEQ IPWER: PATCHIN Ver: 2.0
SEQ ID NO 4
LENTH: 307
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COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FOERS
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 22, Application US/09898883; Patent No. US20020164799A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Adenovirus
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (2)..(307)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-898-883-22
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                                                                                                                                                                                  Sequence 3. Application US/09814292

| Sequence 3. Application US/09814292
| Patent No. US20020120117A1
| Patent No. US20020120117A1
| GENERAL INFORMATION:
| APPLICANT: Yu, De-Chao
| APPLICANT: Yu, De-Chao
| APPLICANT: Yu, De-Chao
| TITLE OF INVENTION: HUMAN URCHELIAL CELL SPECIFIC UROPLAKIN
| TITLE OF INVENTION: HUMAN URCHELIAL REGULATORY SEQUENCES, VECTORS COMPRISING
| TITLE OF INVENTION: WROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
| TITLE OF INVENTION: WROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
| TITLE OF INVENTION: UNDER: US/09/814,292
| CURRENT APPLICATION NUMBER: US/09/814,292
| CURRENT FILING DATE: 2001-10-12
| PRIOR FILING DATE: 2000-03-24
| NUMBER OF SEQ ID NOS: 46
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 3
| LINGTH: 307
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Patent No. US202020136707A1
PERENT. INFORMATION:
APPLICANT: Yu, D.
APPLICANT: Henderson, D.R.
APPLICANT: Schuur, B.R.
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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100.0%; Pred. No. 2.3e-91;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Nucleotide sequence for ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 307; Conservative
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TGATTAA 307
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US-09-814-292-3
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APPLICANT: Little, Andrew
Lamparski, Henry
Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING APPA-FETOPROTEIN AND METHODS OF USE THEREOF
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels
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; Sequence 61, Application US/09151376; Publication No. US20030044383A1
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 307
                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 307; Conservative
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Best Local Similarity 100.
Matches 307; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 TGATTAA 307
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                                                                                              ; FEATURE;
; NAME/KEY: CDS
; LOCATION: (2)..(304)
US-09-151-376-10
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ORGANISM: Unknown
FEATURE:
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SOFTWARE: Patentin Release #1.0, Version #1.30
            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/898,883
FILING DATE: 02-Jul-2001
CLASSIFICATION NUMBER: US/09/898,883
FRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/033,428
FILING DATE: «Unknown-
NAME: POLIZI, CATHERINE M.
REGISTRATION NUMBER: 40,130
REFERENCE/POCKET NUMBER: 34802-30004.00
TELEFAX: (415) 813-5600
TELEFAX: (415) 813-5600
TELEFAX: (415) 813-5600
TELEFAX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STREET CHARACTERISTICS:
LENGTH: 307 base pairs
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Publication No. US20030044383A1
GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REPERBNCE: 34802200021
CURRENT FILING DATE: 1998-09-10
SARLIER FILING DATE: 1996-06-26
EARLIER FILING DATE: 1996-06-26
SARLIER FILING DATE: 1995-06-27
SARLIER PLING DATE: 1995-06-27
NUMBER OF SEQ ID NOS: 71
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100.0%; Score 307; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 2..304
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
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US-09-151-376-10
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     Length 307;
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                                                 Indels
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TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILLE REFERENCE: 34802200221
CURRENT APPLICATION NUMBER: US/09/151,376
CURRENT FILING DATE: 1998-09-10
RAKLIER APPLICATION NUMBER: 08669,753
EARLIER FILING DATE: 1996-06-26
BARLIER FILING DATE: 1995-06-27
NUMBER OF SEQ ID NOS: 71
SOUTHARE: PACENTIN VECTOR OF SEQ ID NOS: 71
LENGTH: 307
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100.0%; Score 307; DB 3;
100.0%; Pred. No. 2.3e-91;
ive 0; Mismatches 0;
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CATGTGGTGGTTTTCCATAGCGCTTATGTTTGCCTTATTATATTATGTGGCTTATTTG 180
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Publication No. US20030068307A1

GENERAL INFORMATION:

APPLICANT: Chen, Yu

APPLICANT: Chen, Yu

APPLICANT: Henderson, Daniel R.

TITLE OF INVENTION: METHODS OF TREATING NEOFLASIA

TITLE OF INVENTION: METHODS OF TREATING NEOFLASIA

TITLE OF INVENTION: METHODS OF TREATING NEOFLASIA

TITLE OF INVENTION: MITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,

TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION

FILE REFERENCE: 348022001600

CURRENT APPLICATION NUMBER: 0S/09/814,357

CURRENT FILING DATE: 2001-01-15

PRIOR FLILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 17

LENGTH: 307
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 307; Conservative
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US-09-814-357-17
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APPLICANT: Lamparski, Henry
Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
THEREOF
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APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
FILE REFERENCE: 348022001700
CURRENT APPLICATION NUMBER: US/09/814,351
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 307
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100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
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; Publication No. US20030026792A1
; GENERAL INFORMATION:
                                      ; Sequence 17, Application US/09814351; Publication No. US20030148520A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                       APPLICANT: Yu, De-Chao
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RESULT 8
US-09-814-351-17
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NAME/KEY: Coding Sequence
LOCATION: 2...304
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
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TOPOLOGY: linear
                               NUMBER OF SEQUENCES: 22
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Sequence 21, Application US/10222479
Publication No. US20030091538A1
GENERAL INFORMATION: Chao
APPLICANT: Yu, De Chao
Schuur, Eric
Henderson, Daniel
TITLE OF INVENTION: ADENOVITENS VECTORS SPECIFIC
FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AACAICTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/045,116

FILING DATE: 23-Oct-2001

CLASSIFTATION ATMA:

APPLICATION NUMBER: US/09/033,555A

FILING DATE: 02/mar-1998

ATTORNEY/AGENT INFORMATION:

NAME: POLICATION NUMBER: 40,130

REGISTRATION NUMBER: 40,130

REGISTRATION NUMBER: 40,130

REGISTRATION NUMBER: 34802-30005.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 2..304
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-045-116-19
                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 434-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNPOERS SFO
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0
Matches 307; Conservative
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100.0%; Score 307; DB 5; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels (
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEE FOR Windows
SOFTWARE: FASTSEE FOR WINDOWS
TOTAL APPLICATION DATA:
APPLICATION NUMBER: US/10/222,479
FILING DATE: 16-Aug-2002
CLASSIFICATION: UNKNOWN>
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/614,495
FILING DATE: 11-0100
APPLICATION NUMBER: 09/033,333
FILING DATE: *CUNKNOWN'>
ATTORNEY/AGRYT INPORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20007.00
TELECOMMUICATION: NUMBER: 50.130
TELEPHONE: 650-813-5600
TELEFRAX: 650-494-0792
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                                                                                                        GENERAL INFURGATION:
APPLICANT: Schuur, E.R.
TITLE OF INVENTAINON: TISSUE SPECIFIC VIRAL VECTORS
FILE REFERENCE: 34802200021
CURRENT APPLICATION NUMBER: US/10/139,089
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 08/69,753
PRIOR APPLICATION NUMBER: 08/69,753
PRIOR APPLICATION NUMBER: 08/69,753
PRIOR APPLICATION NUMBER: 09/509
PRIOR FILING DATE: 1995-06-27
PRIOR APPLICATION NUMBER: 09/509,591
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: 09/033,428
PRIOR APPLICATION NUMBER: 09/033,555
PRIOR APPLICATION NUMBER: 09/033,555
PRIOR APPLICATION NUMBER: 09/033,555
PRIOR APPLICATION NUMBER: 09/033,555
PRIOR APPLICATION NUMBER: 09/033,333
PRIOR APPLICATION NUMBER: 09/039,762
PRIOR PILING DATE: 1999-03-03
PRIOR PILING DATE: 1999-03-03
PRIOR PILING DATE: 1999-03-03
PRIOR PILING DATE: 1999-03-03
PRIOR PILING DATE: 1997-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 307; DB 6; 100.0%; Pred. No. 2.3e-91;
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RESULT 11
US-10-139-089-10
is Sequence 10, Application US/10139089
is Publication No. US20030152553A1
igeneral Information:
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Matches 307, Conservative
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ORGANISM: Homo sapiens
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, LOCATION: (2)..(304)
US-10-139-089-10
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Unknown Organism: Unknown US-10-139-089-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                            APPLICANT: SCHUUT, B.R.

TITLE OF INVENTION: TISSUB SPECIFIC VIRAL VECTORS
FILE REFERENCE: 34962200021
CURRENT PEDLICATION NUMBER: US/10/139,089
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 08/69,753
PRIOR FILING DATE: 1996-06-26
PRIOR FILING DATE: 1995-06-27
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 09/509,591
PRIOR FILING DATE: 1998-09-10
PRIOR PLING DATE: 1998-09-10
PRIOR PLING DATE: 1998-03-02
PRIOR PLING DATE: 1998-03-02
PRIOR PLING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
PRIOR PLING DATE: 1998-03-02
PRIOR PLING DATE: 1998-03-02
PRIOR PPLICATION NUMBER: 09/033,535
PRIOR PLING DATE: 1998-03-02
PRIOR FILING DATE: 1997-03-03
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1997-03-03
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PR
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100.0%; Score 307; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-10-691-045-17
Sequence 17, Application US/10691045
Publication No. US20040146489A1
Sequence 61, Application US/10139089
Publication No. US20030152553A1
GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
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Gaps

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121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTCTTATTATTATATATGTGGCTTATTTG 180
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                                                                                                                                                                                                       100.0%; Score 307; DB 8; Length 307; 100.0%; Pred. No. 2.3e-91; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 307; Conservative
                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 TGATTAA 307
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                                                                                                              ; NAME/KEY: CDS
; LOCATION: (2)..(304)
US-10-822-873-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Unknown
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  SEQ ID NO 10
LENGTH: 307
                                                                                             FEATURE:
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                                   APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Li, Yuanhao
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS RIBOSOME ENTRY SITE
FILE REFERENCE: 348022001700
CURRENT APPLICATION NUMBER: US/10/691,045
CURRENT FILING DATE: 2003-10-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR PLICATION NUMBER: 60/192,156
PRIOR PLICAGO DATE: 2000-33-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 307
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Sequence 10, Application US/10822873

Publication No. US20040241857A1

GENERAL INFORMATION:

APPLICANT: Henderson, D.R.

APPLICANT: Schuur, E.R.

ITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS

FILE REFERENCE: CELL-004CON2

CURRENT APPLICATION NUMBER: US/10/822,873

CURRENT APPLICATION NUMBER: 09/732,169

PRIOR APPLICATION NUMBER: 09/732,169

PRIOR FILING DATE: 2000-12-06

PRIOR APPLICATION NUMBER: 09/151,376

PRIOR PLING DATE: 1996-00-10

PRIOR FILING DATE: 1996-06-26

PRIOR FILING DATE: 1996-06-26

PRIOR FILING DATE: 1996-06-27

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PALENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Nucleotide sequence for ADP US-10-691-045-17
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 307; Conservative
GENERAL INFORMATION:
APPLICANT: Yu, De-Chao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Unknown Organism: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
US-10-822-873-61

Sequence 61, Application US/10822873

Sequence 61, Application US/10822873

GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
FILE REPERENCE: CELL-004CON2
CURRENT APPLICATION NUMBER: US/10/822,873

CURRENT APPLICATION NUMBER: 09/732,169

PRIOR PILING DATE: 2000-12-06
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1996-06-26

PRIOR FILING DATE: 1996-06-26

PRIOR FILING DATE: 1996-06-26

PRIOR FILING DATE: 1996-06-27

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 61

LENGTH: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 307; DB 8; Best Local Similarity 100.0%; Pred. No. 2.3e-91; Matches 307; Conservative 0; Mismatches 0;
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1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT 60

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8 6 8 6 8 6 8

Search completed: January 20, 2006, 21:23:53 Job time : 806 secs

TGATTAN 307 |||||||| TGATTAA 307

7472, Ap 17, Appl

Appl Appl Appl

Sequence

Sequence 5, Appli Sequence 1, Appli Sequence 30, Appli Sequence 28, Appl Sequence 7472, Appl Sequence 17, Appl Sequence 1755, A Sequence 17565, A Sequence 12564, A Sequence 12564, A

Sequence 216, App Sequence 12, Appl Sequence 37, Appl

Sequence 12371, A

13845,

Sequence

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APPLICANT: Yu, De Chao
APPLICANT: Yu, De Chao
APPLICANT: Schuur, Eric
APPLICANT: Schuur, Eric
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
ANDRER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FORESTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                 US-09-952-060-28
US-10-131-827-7472
US-09-244-796-17
US-09-949-016-17565
US-09-949-016-17565
US-09-949-016-13176
US-09-949-016-13176
US-09-549-016-13176
US-09-549-016-13176
US-09-549-18-18-18-18-18-18-18-18-18-18-18-18-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
CITY: Palo Alto
COUNTY: USA
ZIP: 94304-1018
ZUP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: TEM COMPATIBLE
COMPUTER: SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/033,333
FILING DATE: 02-MAR-1998
CLASSIFICATION
PRIOR APPLICATION NUMBER: 40,130
REGISTRATION NUMBER: 40,130
REGISTRATION NUMBER: 40,130
REGISTRATION NUMBER: 34802-20007.00
TELECHOWNICATION INFORMATION:
TELEPHONE: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-13845
US-09-949-016-12371
                                                                                                                                                                                                                                                                                                                              -08-724-394A-12
-09-596-002-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/09033333
Patent No. 6197293
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELERAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                         289
289
116955
                                      35935
35935
35935
35978
36620
37474
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FEATURE:
NAME/KEY: Coding
US-09-033-333-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
; Search time 144 Seconds (without alignments) 3789.663 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Appl
Sequence 22, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                   1 gatgaccggctcaaccatcg.....ttcttttacagtatgattaa 307
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Sequence 1,
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Sequence 10,
Sequence 61,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22
Sequence 9,
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued Patents NA:*

| cgn2 6/ptodata/1/ina/1 COMB.seq:*
| cgn2 6/ptodata/1/ina/5 COMB.seq:*
| cgn2 6/ptodata/1/ina/6A COMB.seq:*
| cgn2 6/ptodata/1/ina/6B COMB.seq:*
| cgn2 6/ptodata/1/ina/H COMB.seq:*
| cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
| cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
| cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
| cgn2 6/ptodata/1/ina/PC COMB.seq:*
| cgn2 6/ptodata/1/ina/PC COMB.seq:*
| cgn2 6/ptodata/1/ina/PC COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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US-09-033-428-22
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US-09-03-614-495-21
US-09-151-376-10
US-09-151-376-10
US-09-151-376-10
US-09-151-376-10
US-09-14-321-17
US-09-14-235-3
US-09-16-351-17
US-09-17-35-30-11
US-09-111-911-5
US-09-111-911-5
US-09-563-863A-3
US-08-563-863A-3
US-08-563-863A-3
US-08-563-863A-3
US-08-563-863A-3
US-08-563-863A-3
US-08-563-863A-3
US-08-563-863A-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                January 20, 2006, 19:14:55
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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STRANDEDNESS: double
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Patent No. 6254662

GENERAL INFORMATION:
APPLICANT: Little, Andrew
APPLICANT: Little, Andrew
APPLICANT: Lemparski, Henry
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: ADBNOVINGS VECTORS SPECIFIC FOR CELLS
TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 23
CORRESPONDENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEB: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                     CATGIGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGTGGCTTATTTG 180
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                                                                             Length 307;
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ZING READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compartible

COMPUTER: DEP PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/033,428

FILING DATE:
                                                                             100.0%; Score 307; DB 3;
100.0%; Pred. No. 1.6e-97;
iive 0; Mismatches 0;
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ATTORNEY/AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 494-0792
TELEFAX: (415) 494-0792
TELEFAX: (415) 494-0792
TELEFAX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
                                                                                  Query Match
Best Local Similarity 100.
Matches 307; Conservative
; LOCATION: 2...304
; OTHER INFORMATION:
US-09-033-333-21
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APPLICANT: TANGERSON, Daniel R.
APPLICANT: Yu, De Chao
TITLE OF INVENTION: ADENOVIUS VECTORS CONTAINING
TITLE OF INVENTION: ADENOVIUS VECTORS CONTAINING
TITLE OF INVENTION: DE USING SAME
TITLE OF INVENTION: OF USING SAME
TITLE OF SEQUENCES: 41
CORRESPONDENCES: ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
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                                                                                                                                            Query Match
Best Local Similarity 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
SOFTWARE: FastSEQ for Windows
APPLICATION NUMBER: US/09/033,556
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ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20010.00
TELECOMMULICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEPHONE: 650-844-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09033556; Patent No. 6432700; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..304
US-09-033-428-22
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Sequence 22, Application US/0989883

Patent No. 6585968

GENERAL INFORMATION:
Little, Andrew
APPLICANT: Little, Andrew
Schuur, Eiic
Henderson, Daniel
TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
EXPRESSING APPA-FETOPROTEIN AND METHODS OF USE THEREOF
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                NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-20007.00
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-494-0792
TELEFAX: 650-494-0792
TELEFX: 706141
INFORMATION POR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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100.0%; Score 307; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0;
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ZIP: 94304-1018
UTER READABLE FORM:
WEDTUM TYPE: Floppy disk
COMPUTTR: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-614-495-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Coding (LOCATION: 2...304) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 TGATTAA 307
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NAME/KEY:
  ATTORNEY/AGENT
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US-09-898-883-22
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US-09-614-495-21
Sequence 21, Application US/09614495
Fatent No. 6436394
GENERAL INFORMATION:
CENTRY, Yu, De Chao
Schuur, Ent.
Comur, Ent.
Henderson, Daniel
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBW Compatible
OPERATING SYSTEM: Windows
SOFTWARE: PRESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        100.0%; Score 307; DB 3;
100.0%; Pred. No. 1.6e-97;
tive 0; Mismatches 0;
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FILING DATE: 11-Jul-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/033,333
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                          NAME/KEY: Coding Sequence
LOCATION: 2...304
// OTHER INFORMATION:
US-09-033-556-9
           INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
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Best Local Similarity 100.
Matches 307; Conservative
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FEATURE:
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100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/033,428
FILING DATE: <unknown>
ATTORNEY AGENT INFORMATION:
NAME: POLIZZI, CATHERINE M.
REGESTRATION NUMBER: 40,130
REFERENCS/DOCKET NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 494-0792
TELEFAX: (415) 494-0792
ITELEFAX: 706141 WRSNFORRS SFO
INFORMATION FOR SEQ 1D NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09151376
Sequence 10, Application US/09151376
Sequence No. 6676935
GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
APPLICANT: Schuur, E.R.
TILE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REPERENCE: 34802200021
CURRENT APPLICATION NUMBER: US/09/151,376
CURRENT FILING DATE: 1996-06-26
EARLIER FILING DATE: 1996-06-26
EARLIER FILING DATE: 1995-06-27
EARLIER PILING DATE: 1995-06-27
NUMBER OF SEQ ID NOS: 71
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,883
FILING DATE: 02-011-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 2..304
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                           LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                 Length 307;
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; Sequence 61, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.;
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER FILING DATE: 1996-06-26
; EARLIER PILING DATE: 1996-06-26
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NOS: 71
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Pred. No. 1.6e-97;
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100.0%; Score 307; D
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 307; Conservative 0; Mismatches
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 307
                                                                  TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(304)
US-09-151-376-10
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ORGANISM: Unknown
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100.0%; Score 307; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Nucleotide sequence for ADP US-09-814-292-3
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATGTGGCTTATTTG 180
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09814351
| Patent No. 6692736
| GENERAL INFORMATION:
| APPLICANT: Yu, De-Chao
| APPLICANT: Yu, De-Chao
| APPLICANT: Li, Yuanhao
| APPLICANT: Henderson, Daniel R.
| TITLE OF INVENTION: CCMPRISING AN INTERNAL RIBOSOME ENTRY SITE
| FILE REFERENCE: 348022001700
| CURRENT APPLICATION NUMBER: US/09/814,351
| PRIOR PILING DATE: 2001-03-21
| PRIOR PILING DATE: 2001-03-24
| NUMBER OF SEQ ID NOS: 35
| SOFTWARE: RastSEQ for Windows Version 4.0
| SEQ ID NO 17
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100.0%; Score 307; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Nucleotide sequence for ADP US-09-814-351-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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TGATTAA 307
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US-09-814-351-17
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Sequence 3, Application US/09814292
; Sequence 3, Application US/09814292
; Patent No. 685258
; GENERAL INPORMATION:
 APPLICANT: The Chao
; APPLICANT: Abang, Hong
; APPLICANT: Honderson, Daniel R.
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
; TITLE OF INVENTION: HERTHODS OF USE THEREOF
; TITLE OF INVENTION: WROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
; TITLE OF INVENTION: WRETHODS OF USE THEREOF
; TITLE OF INVENTION: WRETHODS OF USE THEREOF
; FILE REFERENCE: 346022001500
; CURRENT APPLICATION NUMBER: G0/191,861
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PASISEQ for Windows Version 4.0
; SEQ ID NO 3
: LENGTH: 307 Sequence 7, Application US/0939282A
Petent No. 6900049
GENERAL INFORMATION:
APPLICANT: YU, De Chao
APPLICANT: Henderson, Daniel
TITLE OF INVENTION: Adenovirus Vectors Containing Cell
TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
FILE REFERENCE: CELL-014; 122.1
CURRENT APPLICATION NUMBER: US/09/392,822A
CURRENT FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: 60/099,791
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09 120 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGGGGCTTGGA 120 121 CATGIGGIGGITITCCATAGCGCTTATGTTTGTTTTGCCTTATTATATGTGGCTTATTTG 180 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATTATTGT 180 181 TIGCCTAAAGCGCAGACGCCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC 240 241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300 241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300 1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACACTGCTACCGGACT 60 1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT 61 AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA Gaps ö Length 307;

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241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
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Patent No. 6916918
GENERAL INFORMATION:
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LOCATION: (2)..(307)
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LENGTH: 307
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Patent No. 6911200

GENERAL INFORMATION:
APPLICANT: Chen, Yu
APPLICANT: Henderson, Daniel R.
TITLE OF INVENTION: MITH COMBINATION TRAGET CELL-SPECIFIC ADENOVIRUS,
TITLE OF INVENTION: GENOCHHERAPY AND RADIATION
FILE REFERENCE: 348022001600
CURRENT APPLICATION NUMBER: 05/09/814,357

CURRENT PILING DATE: 2001-10-15
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35

SEQ ID NO 17

LEMECTHER FASTERE FOR WINDOWS VERSION 4.0

SEQ ID NO 17

LEMECTHER FASTERE FOR WINDOWS VERSION 4.0

SEQ ID NO 17

LEMECTHER FASTERE FAST
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100.0%; Pred. No. 1.6e-97;
tive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 307; Conservative
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                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (20)...(304)
US-09-392-822A-7
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Best Local Similarity
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                                                                                                                         TYPE: DNA
ORGANISM: Adenovirus
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                                                                                             LENGTH: 307
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APPLICANT: W. D. D. R.
APPLICANT: Henderson, D.R.
APPLICANT: Henderson, D.R.
TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
TITLE OF INVENTION: BUNDBER: US/09/875,228
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/127,834
PRIOR APPLICATION NUMBER: 09/127,834
PRIOR APPLICATION NUMBER: 60/076,545
PRIOR APPLICATION NUMBER: 60/076,545
PRIOR APPLICATION NUMBER: 60/076,545
PRIOR APPLICATION NUMBER: 60/056,545
PRIOR APPLICATION NUMBER: 60/056,545
PRIOR SELING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
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61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA
                                                                                                   121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGCCTTATTATTATGTGGCCTTATTTG
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100.0%; Score 307; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0;
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Query Match 63.8%; Score 196; DB 3; Best Local Similarity 86.4%; Pred. No. 1.7e-57; Matches 228; Conservative 0; Mismatches 35
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Patent No. 6835812
                                                                                                                                                    Query Match
Best Local Similarity 99.33
Matches 305; Conservative
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US-09-562-930-11
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241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
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US-09-111-911-5/c
Sequence 5, Application US/09111911
Patent No. 6881402
GENERAL INFORMATION:
TITLE OF INVENTION: Inhibiting Apoptosis With Adenovirus RID Protein
FILE REPRENCE: 16153-587
CURRENT APPLICATION NUMBER: US/09/111,911
CURRENT FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 5
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100.0%; Score 307; DB 3; Length 35937;
Best Local Similarity 100.0%; Pred. No. 1.9e-96;
Matches 307; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                         Sequence 3, Application US/09782378A
; Sequence 3, Application US/09782378A
; Patent No. 6916635
; GENERAL INFORMATION:
    APPLICANT: Hearing, Patrick
    APPLICANT: Bahou, Wadie
    APPLICANT: Sandalon, Ziv
    APPLICANT: Gantenko, Dmitri
    ITLE OF INVENTION: Adenoviral Vectors
    FILE REFERENCE: STONYB-04970
    CURRENT APPLICATION NUMBER: US/09/782,378A
    CURRENT PILING DATE: 2001-02-12
    PRIOR FILING DATE: 2000-10-02
    NUMBER OF SEQ ID NOS: 27
    SOFTWARE: PatentIn version 3.0
    SEQ ID NO 3
    LENGTH: 35937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA; Human adeno-associated virus 2 US-09-782-378A-3
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US-09-782-378A-3
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APPLICANT: Genotherapeutics Inc.
APPLICANT: Genotherapeutics Inc.
APPLICANT: Steiner, Mitchell
APPLICANT: Steiner, Mitchell
APPLICANT: Wang, Chiang
APPLICANT: Wang, Chiang
APPLICANT: Menon, Rema
APPLICANT: Menon, Rema
TITLE OF INVENTION: Isolated nucleic acids of the p-hyde family, p-hyde proteins, and
TITLE OF INVENTION: of inducing susceptibility to induction of cell death in cancer;
FILE REFERENCE: P-2762-US2
CURRENT PELLING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: US 09/302,457
PRIOR APPLICATION NUMBER: US 09/499,817
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 32166
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Plasm
OTHER INFORMATION: Combining E.coli and Adenovirus Sequences
                                                                                                                                                                                                                                                                              Indele
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	284 TCTCTTCTTTTACAGTATGATTAA 307	284	ò
26419	26360 TCATTGTGCTACACCCAAACAATGATGGAATCCATAGATTGGACGGAC	26360	qq
283	225 TCATTGTGCTCAAACCCACACAATGAAAAATTCATAGATTGGACGGTCTGAAAC-CATGT 283	225	È
26359	26300 TTATGIGGCTCATCTGCTGCTGAAAGGCGAACGCGCCCGACCACCCATCTATAGTCCCA 26359	2630(ą
224	165 TTATGTGGCTTATTTGTTGCCTAAAGCGCAGACGCCGCAGCCAGC	165	ò
26299		2624(qq

Search completed: January 20, 2006, 21:10:15 Job time : 147 secs

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January 20, 2006, 17:03:15 ; Search time 472 Seconds (without alignments) 4334.874 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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307
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aav47675 Adenoviru	Aav52966 Adenoviru	Aav57354 Adenoviru	Aax24756 DNA encod	Aaz99937 DNA encod	Aai70186 Adenoviru	Aah43535 ADP nucle	Abk99587 DNA encod	Acd07312 DNA encod	Adi36397 Human muc	Adi36417 DNA encod	Adv21029 Human muc	Adv20978 Adenoviru	Adw47774 Adenoviru	Adw28317 Partial D	Abk49009 Adenovira	Adw28315 DNA seque	Abs69881 Human ade	Acc70007 Nucleotid
ΩΙ	AAV47675	AAV52966	AAV57354	AAX24756	AAZ99937	AAI70186	AAH43535	ABK99587	ACD07312	ADI36397	ADI36417	ADV21029	ADV20978	ADW47774	ADW28317	ABK49009	ADW28315	ABS69881	ACC70007
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New adenovirus vector, for treating cancers - comprising an adenovirus gene under the transcriptional control of an alpha fetoprotein transcription regulatory element.

Claim 31; Page 74; 102pp; English.

Little AS, Lamparski HG, Henderson DR, Schuur ER;

WPI; 1998-495861/42. P-PSDB; AAW61197.

XIXEEXITIX

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	21	305.4	99.5	307	7 N	AAU58003 AAV53632	Aaq68003 Ad2/-Okr6 Aav53632 Adenoviru
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υ	2 4	303	9.6	34427	7 4	ADM2839 ADW28319	Adau9839 Adenoviru Adw28319 Nucleotid
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	26	302.2	98.4	35759		ADS00148	Ads00148 Human ade
	28	196	63.8	32165		AAA14723	Aaa14723 Nucleotid
	53	196	63.8	32166		AAA09090	Aaa09090 AdPSA-bet
	30	196	8.6	32166		AAC89170	Aac89170 AdRSVpHYD
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	33	196	63.8	32167		AAZ93332	Aaz9332 Partial s
	34	196	63.8	32886		AAA09086	Aaa09086 AdRSV-bet
	32	196	63.8	33592		AAC85018	Aac85018 Adenoviru
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	38	196	63.8	34302		AAZ94163	Aaz94163 Adenoviru
	39	196	63.8	34341		AAC85019	Aac85019 Adenoviru
	40	196	63.8	34448		AAC85021	Aac85021 Adenoviru
	41	196	63.8	34737		AAC85024	Aac85024 Adenoviru
	42	196	63.8	35408		AAT59272	Aat59272 Recombina
	4 4 4 4	1 26	8.0	35620		ADY80723	Ady80723 DNA seque
	45	196	63.8	35712		ADZ45246	Adz45246 Human ade
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ž ž ž	Ader	Adenovirus death protein; ADP; alpha-fetoprotein transcriptio	death _] protein	protein transc	, AL ript	vector; he n regulator	er; FP-TRE;
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113	Key		707	ocation 307	/Qua a	Location/Qualifiers 2307 /*tag= a	
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4	(G	(CALY-) CAI	CALYDON INC	ŠČ.			

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This is the coding region of the adenovirus death protein (ADP, see AAW78902). It can be obtained by PCR amplification (see also AAV52945-46). Claimed replication-competent adenovirus (Ad) vectors comprise an Ad gene under transcriptional control of a CEA-TRE. The vectors can be used to detect and monitor samples for the presence of cells that allow a CEA-TRE to function, and to selectively kill such cells, especially malignant cells. Vectors containing an ADP gene may be more potent than vectors dosage requirement
                                                                                                                                                                      New adenovirus vectors, particularly for cancer therapy - comprising adenovirus gene under transcriptional control of carcinoembryonic antigen transcriptional regulatory element.
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                                                                            Schuur ER;
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                                       (CALY-) CALYDON INC
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02-MAR-1998;
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                                   AW61197) of adenovirue type 2. The ADP coding sequence (with or without the Y leader) can be introduced into an adenoviral genome, e.g. in the E3 or E4 region. Inclusion of such a coding sequence in an adenoviral vector significantly enhances the extent of cytocoxicity, cell killing and virus production. The invention provides replication-competent adenovirus vectors which preferentially replicate in cells that express alphatetoprotein (AFP), particularly hepatoma cells. The vectors comprise at least one adenovirus gene, preferably a gene that contributes to cytocoxicity, under the transcriptional control of an AFP transcription conferring selective cytocoxicity to AFP-expressing cells, especially cancer cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATGIGGTGGTTTTCCATAGCGCTTATGTTTGCCTTATTATATTATGTGGCTTATTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGACCGGCTCAACCGTCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                         GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                      nucleotide sequence codes for adenovirus death protein (ADP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carcinoembryonic antigen; transcriptional regulatory element, human; promoter; enhancer; vector; cancer; gene therapy; PCR; adenovirus death protein; ADP; ds.
                                                                                                                                                                                                                                                                                                                                          Length 307;
                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                    Seguence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 307; DB 2; 100.0%; Pred. No. 2.4e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adenovirus death protein gene coding region.
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Matches 307; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409839467-A2
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New adenovirus vectors, particularly for cancer therapy - comprising an adenovirus gene under transcriptional control of a probasin transcriptional regulatory element.
                                                                                                                                                          Disclosure, Page 96; 117pp; English.
                                                                                              Schuur ER,
                                                           97US-0039762P
98US-00033333
                                               98WO-US004132
                                                                                              Henderson DR,
                                                                                                            WPI; 1998-506369/43.
                                                                                (CALY-) CALYDON INC
                                                                                                                 P-PSDB; AAW75787
                                               03-MAR-1998;
                                                            03-MAR-1997;
02-MAR-1998;
                    WO9839466-A2
                                 11-SEP-1998
                                                                                              Υu D,
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Lamparski HG;

This is the coding region of the adenovirus death protein (ADP, see AAW5787). It can be obtained by PCR amplification (see also AAV57350-51). Claimed replication-competent adenovirus (Ad) vectors comprise an Adgene under transcriptional control of a probasin transcriptional response element (PB-TRE, see AAV57334). The vector can be used for detecting calls that allow a PB-TRE to function, especially cells expressing an androgen receptor, such as prostate cells. They can be used to confer selective toxicity to such cells. In particular, the vectors can be used for treating cancers such as prostate cancer. Ad vectors can be used for treating cancers such as prostate cancer. Ad vectors can be used for treating cancers such as prostate cancer. Ad vectors can be used fective treatment and/or a lower dosage requirement. An Ad vector has been constructed that contains the ADP gene under control of PB-TRE. Cytotoxicity was demonstrated toward LNCaP (prostate carcinoma) cells Gaps ö 100.0%; Score 307; DB 2; Length 307; 100.0%; Pred. No. 2.4e-94; 0; Indels Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other; 0; Mismatches Query Match Best Local Similarity 100.º Matches 307; Conservative

61 AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATGTGGCTTATTTG 180 121 CATGTGGTGTTTTCCATAGCGCTTATGTTTGCCTTATTATTATGTGGCTTATTTG 180 1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT 61 121 셤 ò 셤 ઠે 셤

240 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTCTTTTACAGTA 300 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300 TTGCCTAAAGCGCAGACGCCCCAGACCCCCATCTATAGGCCTATCATTGTGCTCAACCC TGATTAA 307 181 301 241 유 ò 셤

TTGCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC 240

181

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TGATTAN 307

301

AAX24756 standard; DNA; 307 RESULT 4
AAX24756
ID AAX2

Enhancer; glandular kallikrein-1; hGK-1; hKLK2; human; prostate cancer; therapy; adenovirus death protein; ss. 309
 /*tag= a
 /product= "adenovirus death protein" DNA encoding adenovirus death protein. Location/Qualifiers 97US-0054523P. 98US-0076545P. 98US-00127834. 98WO-US016312 (first entry) Human adenovirus type 2. (revised) W09906576-A1 04-AUG-1998; 04-AUG-1997; 02-MAR-1998; 03-AUG-1998; 17-OCT-2003 21-JUN-1999 11-FEB-1999 AAX24756;

New nucleic acid containing the human glandular kallikrein enhancer - providing increased expression of heterologous sequences in prostatic cells, and related adenoviral vectors for treating prostatic cancer. WPI; 1999-153804/13. P-PSDB; AAW98003.

Schuur ER;

Herdenson DR,

Yu D,

(CALY-) CALYDON INC

Disclosure; Page 165; 179pp; English

This polynucleotide encodes the adenovirus death protein (ADF, see AAW98003) of adenovirus serotype 2. The invention provides novel adenovirus vectors in which at least one adenovirus gene, preferably one that contributes to cytocoxicity, is placed under transcriptional control of a human glandular kallikrein hKLK2 enhancer transcriptional regulatory element (hKLK2-TRE, see AAX24755). Such vectors are useful for treatment of cancers such as prostate cancer. The ADP gene may render the adenoviral vector more potent, making possible more effective treatment and/or lower dosage regulirement. (Updated on 17-OCT-2003 to standardise OS field)

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Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

ö 120 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGGCGAGCTTGGA 120 180 121 cardresiderririccaraccerrarerrirerrisecriarrarrarere 180 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC 240 9 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCCACTGCTACCGGACT 1 dargaccedercaaccarcececeacaaceacrarcecaacaccacrecrecreceacr 61 AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGCTTATTTG 0; Gaps ; Score 307; DB 2; Length 307; Pred. No. 2.4e-94; 0; Mismatches 0; Indels (100.0%; Query Match Best Local Similarity 100.' Matches 307; Conservative 121 셤 g 셤

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61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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AAI70186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes an adenoviral death protein, which is used to construct the vectors of the invention. The specification describes adenoviral vectors which comprise an adenovirus gene under transcriptional control of a cell status specific transcriptional regulatory element (TRE). The TRE is preferably one that is essential for adenovirus proteins and propagation. The adenovirus vectors may be used for the treatment of a range of tumours such as lung, stomach, breast, colon and rectum, and uterine and cervix cancers
                300
                               241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
                  ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adenovirus vectors comprising cell-status specific response elements useful in gene therapy protocols for the treatment of cancers.
                                                                                                                                                                                                                                                                            adenoviral vector, adenovirus gene; transcriptional control;
transcriptional regulatory element; TRE; adenoviral propagation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 307; DB 3;
100.0%; Pred. No. 2.4e-94;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "death protein"
                                                                                                                                                                                                                                                  DNA encoding an adenoviral death protein.
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 2. .307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 9; 79pp; English
                                                                                                                                                                  AAZ99937 standard; DNA; 307 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US020718
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                        death protein; tumour; ss
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nes 307; Conservative
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                                                                      TGATTAA 307
                                                                                                 TGATTAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-271456/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CALY-) CALYDON INC.
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                                                                                                                                                                                                                                                                                                                                   Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                              WO200015820-A1
                                                                                                                                                                                                                       25-JUL-2000
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                                                                                                                                                                                              AAZ99937;
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The present sequence is that of the coding region of the adenovirus death protein. The sequence was obtained by PCR amplification and used in the construction of adenoviral vectors in which ApP expression was under the control of a urothelial cell-specific transcriptional regulatory element (TRE) derived from the human uroplakin II gene 5' flanking region (see AAI70144). This is an example of adenoviral vectors of the invention. Such vectors comprise a gene, preferably an adenovirus gene, under transcriptional control of a urothelial cell-specific TRE. They display urothelial cell-specific cytocoxicity, and are used for the specific, etargeted gene therapy of bladder cancer. (Updated on II-SEP-2003 to
                                                                                                                                       300
                             121 CATCTGGTGGTTTTCCATAGCGCTTATGTTTGCCTTATTATTATGTGGCTTATTTG 180
                                                                   240
                                                                                     Adenovirus death protein; uroplakin II; vector;
transcriptional regulatory element; TRE; urothelial cell; bladder cancer;
                                                                                                                                                                       241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTTTTTTTACAGTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human urothelial cell specific uroplakin transcriptional regulatory sequences, useful for producing adenoviral vectors which can be used to confer selective cytotoxicity to target cells, especially bladder cancer
121 CATGREGIGGITITCCADAGCGCIDATGITIGITIGCCTATIATATGIGGCTTAITG
                                                                 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
                                                                                                                                        ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adenovirus death protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang H, Henderson DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001WO-US009224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-2000; 2000US-0191861P.
                                                                                                                                                                                                                                                                                                                                      AAI70186 standard; DNA; 307
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adenovirus type 2.
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/*tag=
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P-PSDB; AAM50206.
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07-JAN-2002
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61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120

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This sequence encodes adenoviral ADP. This coding sequence may be used in the replication-competent adenoviral vector (A) of the invention which contrains two genes (G1, G2) that are co-transcribed as a single mRNA and under control of a heterologous, target cell-specific transcriptional regulatory element (TRE). G2 has a mutation in, or deletion of, its endogenous promoter and is controlled from an internal ribosome entry atte (IRES). The ADP coding sequence may be used as G1 or G2. (A) has greater specificity for a target cell than a similar vector in which TRE is operably linked to a gene and which lacks an IRES. (A) are used to modify the genotype of target cells, optionally in vitro with subsequent return of altered cells to the host and where G2 is a cytotoxic gene, to confer selective cytotoxicity to target cells, especially for killing cancer cells. ADP displays a cytotoxic, particularly cell lysis, function. Also (A) are used for diagnosis and monitoring, e.g. detection of bladder cancer cells. The target cell-specific TRE ensures that (A) has better target cells producing such production of adenoviral cells, so a runaway infection is prevented but production of adenoviral proteins in target cells activates and/or stimulates the immune response than two identical control elements) eliminates the risk of homologous recombination and may provide enough extra space for an additional control elements) eliminates the risk of homologous cells in the combination and may provide enough extra space for an additional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TTGCCTAAAGCGCAGACGCCCAGACCCCCATCTATAGGCCTATCATTGTGCTCAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding adenovirus death protein (ADP).
Disclosure; Fig 9; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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Matches 307; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Replication-competent adenoviral vector, useful e.g. for killing cancer cells, contains two genes linked by internal ribosome entry site and controlled by target-specific regulator.
                                                                                                                                                                                                                                                                                                                                                                                    CATGTGGTGGTTTTCCATAGCGCTTATGTTTGCCTTATTATTATGTGGCTTATTG
                                                                                                                                                                                        GATGACCGGCTCAACCATCGCGCCCCACAACGGACTATCGCAACACCACTGCTACCGGACT
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                                                                100.0%; Score 307; DB 4; Length 307; 100.0%; Pred. No. 2.4e-94; ive 0; Mismatches 0; Indels
                      Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
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Matches 307; Conservative C
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(first entry)
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07-JAN-2002
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The present invention relates to adenoviral vectors comprising an adenovirus gene under transcriptional control of a cell type-specific transcriptional response element (TRE). Example TRES given in the specification include human prostate-specific antigen (PSA) TRE, human glandular kallikrein (hKLK) TRE, rat probastin (PB) TRE, human carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3 (WUC1) TRE. The modified adenovirus vector is useful as a vehicle for introducing new genetic capability, particularly associated with cytotoxicity for treating neoplasia. For example, the vector may be used in a target cell to suppress tumour growth, or to kill the target cell. The vector is particularly useful in gene therapy. The present sequence encodes adenovirus death protein (ADP). (Updated on 27-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT
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                                                                                 Adenoviral vector; adenovirus gene; transcriptional control; TRE; cell type-specific; transcriptional response element; PSA; hKLK; prostate-specific antigen; glandular kallikrein; probastin; PB; carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUC1; cytotoxicity; neoplaais; tumour growth; gene therapy; cytostatic; adenovirus death protein; ADP; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
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Pred. No. 2.4e-94;
0; Mismatches 0;
                                          DNA encoding adenovirus death protein (ADP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encodes adenovirus death protein (ADP)
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96US-00599753.
97US-0039597P.
97US-0039762P.
97US-0039763P.
98US-00033428.
98US-00033428.
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07-AUG-2003 (first entry)
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les 307; Conservative
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                                                                                                                                                                                                                                                unidentified adenovirus.
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P-PSDB; ABU10308.
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03-MAR-1997;
03-MAR-1997;
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03-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an adenovirus vector (AV) comprising an AV gene under transcriptional control of a cell type-specific transcriptional regulatory element (TRE) and optionally a first AV gene under control of a first cell type-specific TRE and a second gene under control of second cell type-specific TRE, where the first and second cell type-specific TRE, where the first and second cell type-specific TRE, where the first and second cell type-specific TREs are substantially identical. When the vector is incroduced into a cell (e.g. prostate cell, liver cell, breast cancer cell) in allows the cell type-specific TRE to function, resulting in cycotoxicity. The vector is useful for suppressing tumour growth of a target cell. This sequence represents a polynucleotide used in the scope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                            Novel adenovirus vector comprises adenovirus gene under transcriptional control of cell-type specific transcriptional response element for conferring selective toxicity on target cell and for suppressing tumor
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                                                                                                                                                                                                                                                  Henderson DR, Schuur ER;
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nes 307; Conservative
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                                                                                                                                                                                                      SCHUUR B R.
                                                                                                                                                                                                                                                                                            WPI; 2002-582468/
P-PSDB; ABG69353
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of the invention
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                                              06-JUN-2002
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                       cell type-
proliferations other than tumours, such as psoriatic lesions and wound healing. In addition, it is useful for detecting cells where a cell type specific TRE is functional in a blological sample and for treating prostate-associated diseases such as hyperplasta and cancer. As such, these compositions exhibit cytostatic, antipsoriatic and vulnerary activities. This polymucleotide sequence is the human mucin (MUC1) TRE DNA sequence of the invention. NOTE: This sequence is identical to that given as SeqID 10.
                                                                                                                                                                                                                                                                                                                                                                                           61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA
                                                                                                                                                                                                                                                                                                                 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCCACTGCTACCGGACT
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                                                                                                                                                                                                                                                                                           1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                             100.0%; Score 307; DB 12; Length 307; 100.0%; Pred. No. 2.4e-94;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                           Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding the human ADP protein SeqID10.
                                                                                                                                                                                                                                                     0; Mismatches
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96US-00669753.
97US-0039597P.
97US-0039762P.
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/product= '
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                                                                                                                                                                                                                                                     Matches 307; Conservative
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                                                                                                                                                                                                                                 Local Similarity
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26-JUN-1996;
03-MAR-1997;
03-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel composition that contains a replication competent adenovirus capable of transfecting target host cells. Specifically, it comprises an adenoviral gene essential for replication (ElA, ElB or E4), which is under the transcriptional control of a prostate specific transcriptional response element (TRE) and polyethylene glycol (PEG) as the masking agent. The present invention describes this composition as useful for suppressing tumour cell growth and for lowering the levels of tumour cell markers. It can also be used for introducing transient expression that may be involved in treating undesired
                                                                               240
                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition comprising replication competent adenovirus having adenovirus gene essential for replication under transcriptional control of cell type specific transcriptional response element and masking agent.
                                                                                                                                     CATGTGGTGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATGTGTGGCTTATTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; mucin; MUCl; human; prostate; transcriptional response element; TRE; polyethylene glycol; PGG; masking agent; tumour cell growth; proliferation; psoriatic lesion; wound healing; hyperplasia; cancer; cytostatic; antipsoriatic; vulnerary; human.
                                                                 TTGCCTAAAGCGCAGACGCCCAACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
                                                                                                                 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA
                                       TTGCCTAAAGCGCAGACGCGCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human mucin (MUC1) transcriptional response element DNA SeqID61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; SEQ ID NO 61; 115pp; English.
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96US-00669753.
97US-0039597P.
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97US-0033762P.
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98US-00033555.
98US-00151376.
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LAMPARSKI H G.
HENDERSON D R.
                                                                                                                                                                                             TGATTAA 307
                                                                                                                                                                                                                               TCATTAN 307
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03-MAR-1997;
03-MAR-1997;
02-MAR-1998;
02-MAR-1998;
02-MAR-1998;
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(LITT/) (LAMP/)

Vector; gene transfer; cloning vehicle; genetic engineering; prostate cancer; gene therapy; vaccine; cytostatic; TRE; transcriptional regulatory element; PSE; prostate specific enhancer; PSA; prostate specific antigen; cancer; ds; mucin like glycoprotein DF3; MUCl.

95US-00495034

27-JUN-1995;

13-APR-2004; 2004US-00822873

US2004241857-A1.

02-DEC-2004

Homo sapiens

26-JUN-1996; 96US-00669753. 10-SEP-1998; 98US-00151376. 06-DEC-2000; 2000US-00732169.

(HEND/) HENDERSON D R.

(SCHU/) SCHUUR B R.

Schuur ER,

denderson DR,

WPI; 2005-011642/01

Human mucin like glycoprotein DF3 (MUC1) TRE DNA

(first entry)

24-FEB-2005

ВР

ADV21029 standard; DNA; 307

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This invention relates to a novel composition that contains a replication competent adenovirus capable of transfecting target host cells.

Specifically, it comprises an adenoviral gene essential for replication (ELA, ELB or EA), which is under the transcriptional control of a prostate specific transcriptional response element (TRE) and polyethylene glycol (PEG) as the masking agent. The present invention describes this composition as useful for suppressing tumour call growth and for lowering the levels of tumour cell markers. It can also be used for introducing transient expression that may be involved in treating undesired proliferations other than tumours, such as psoriatic lesions and wound paraling. In addition, it is useful for detecting cells where a cell type-specific TRE is functional in a biological sample and for treating prostate-associated diseases such as hyperplasia and cancer. As such, these compositions exhibit cytostatic, antipsoriatic and vulnerary activities. This polymucleotide sequence is the DNA encoding the human ADP protein of the invention. NOTE: This sequence is identical to that
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                                                                                                                                                                                                                  Henderson DR, Schuur ER,
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 10; 115pp; English
98US-00033428.
98US-00033428.
98US-00033555.
98US-00151376.
                                                                              02-JUN-2000; 2000US-00509591
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Best Local Similarity 100.0
Matches 307; Conservative
                                                                                                                                                                                                                  sittle AS, Lamparski HG,
                                                                                                                    LITTLE A S.
LAMPARSKI H G.
HENDERSON D R.
SCHUUR E R.
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P-PSDB; ADI36347.
                      02-MAR-1998;
02-MAR-1998;
10-SEP-1998;
    02-MAR-1998;
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New adenovirus vector comprising an adenovirus early gene essential for propagation under the control of a human prostate specific antigen promoter and a human prostate specific antigen enhancer, for treating

Example 5; SEQ ID NO 61; 112pp; English.

prostate cancer.

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The present invention relates to an adenovirus vector comprising an adenovirus early gene essential for propagation under the control of a human prostate specific antigen promoter and a human prostate specific antigen promoter and a human prostate specific antigen (PSA) enhancer. The invention is useful for treating a patient suffering from prostate cancer and for making mammalian hosts that are transiently transgenic and for detecting the presence of cells that permit the function of a cell type-specific transcriptional regulatory element (TRE) in a sample. The invention is also used in the gene therapy and also as vaccine. The present sequence is the human mucin like glycoprotein DF3 (MUCI)TRE DAM. This sequence is used to construct replication competent prostate-specific attenuated adenoviruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
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Matches 307; Conservative
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61 AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene therapy; vector; prostate tumor; cytostatic; vasotropic; vulnerary; antipsoriatic; antimicrobial; immunomodulator; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New replication competent adenovirus vector comprising an inducible transcriptional transactivator coding sequence and an adenovirus gene, useful for treating cancer, psoriatic lesions, restenosis or wound
                                                                      1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACACCACTACCGGACT
                                                                                                                                                                                                                     CATGIGGIGGITITICCATAGCGCTTATGTTTGTTTTGCCTTATTATTATGTTTTTT
                                           1 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT
                                                                                                                                                                                                                                                                                                         181 TIGCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adenovirus death protein coding sequence.
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307; Conservative
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                      ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
                                        Vector; gene transfer; cloning vehicle; genetic engineering; prostate cancer; gene therapy; vaccine; cytostatic; prostate-specific antigen; TRE; transcriptional regulatory element; PSE; prostate specific enhancer; PSA; prostate specific antigen; cancer; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New adenovirus vector comprising an adenovirus early gene essential for propagation under the control of a human prostate specific antigen promoter and a human prostate specific antigen enhancer, for treating prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Adenovirus death protein (ADP)"
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                                                                                                                                                                                                                                                                                                                                                                                             Adenovirus death protein (ADP) encoding DNA
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2. .307
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                                                                                                                                                                                                                                                              ADV20978 standard; DNA; 307 BP.
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26-JUN-1996; 96US-00669753.
10-SEP-1998; 98US-00151376.
06-DEC-2000; 2000US-00732169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-2004; 2004US-00822873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unidentified adenovirus.
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                                                                                                        TGATTAA 307
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100.0%; Score 307; DB 14; Length 307; 100.0%; Pred. No. 2.4e-94;

Query Match Best Local Similarity

ganciclovir; AdS-yCD/mutTK(SR39)rep-ADP; 88.

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agent. The adenovirus gene is preferably a gene essential for adenoviral agent. The adenovirus gene is preferably a gene essential for adenoviral agent. The adenovirus gene is preferably a gene essential for adenoviral captured by the inducing agent. Also claimed is an adenovirus vector comprising; an inducible TT coding sequence under transcriptional control of a TRE regulated by the TT and a genous under transcriptional control of a genoud gene may an adenovirus gene under transcriptional control of a second TRE, where the TT ad adenoviral gene essential for adenovirus replication, or a transgene such as a cytotoxic gene. One embodiment of the invention provides adenovirus or as a cytotoxic gene. One embodiment of the invention provides adenovirus as a cytotoxic gene. One embodiment of the invention provides adenovirus control of a second transactivator regulated TRE, where the condenovirus gene is essential for replication. Also claimed are host cells comprising the replication competent adenovirus vector, and methods for propagating and regulating the vector. A claimed methods for propagating and regulating the vector. A claimed method for selective cytolysis of a target tumor cell line involves introducing the adenovirus vector an inducing agent such that the adenovirus vector can also be created propagate prostate cells. The adenovirus vector can also be created transcriptions, restenosis, wound healing, tissue crepair, enhanced immune response, resistance to infection, production of factors, enhanced immune response, resistance to infection, production of factors, enhanced immune response, resistance to infection, production of factors, enhanced immune response, resistance to infection, production of factors, enhanced immune response, resistance to infection, production of the created poth by the CTTRE to demonstration of metabolic or other physiological pathways, or comparison of a viral gene essential for replication is regulated both by the control of the invention, expression of the viral gene essent
control of a TRE regulated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 indirectly by the concentration of the inducing agent
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Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

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240
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                                                                                                                            CAIGIGGIGGITITICCATAGCGCITAIGITIGITIGCCITATIAITATGTGCCTTATITG 180
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                                                      GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCCCTCTTACCGGACT 60
                                                                               9
                                                                    GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGACT
                                                                                                                                                                                        CATGTGGTGGTTTTCCATAGCGCTTATGTTTGCTTTATTATTATGTGGCTTATTTG
                                                                                                                                                                                                                    TTGCCTAAAGCGCAGACGCCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
                             Gaps
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0
 100.0%; Score 307; DB 14; Length 307; 100.0%; Pred. No. 2.4e-94;
                           Indels
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                           Matches 307; Conservative
Query Match
Best Local Similarity
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The specification describes a polynucleotide comprising a nucleotide sequence of yeast cytosine deaminase/mutant SR39 herpes simplex virus type 1 thymidine kinase fusion gene, and further comprising an adenovirus type 5 adenovirus death protein gene. The polynucleotide of the invention limits the side effects of cancer treatment by using only lower doses of radiation. The polypeptide encoded by the above polynucleotide is useful for converting 5-fluorocytosine or ganciolovir into active chemotherapeutic agents. Pharmaceutical compositions comprising useful for treating a mammalian patient having a malignancy or solid tumor. The present sequence represents a partial sequence (the E3 region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTTACAGTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATGLGGTGTTTTCCATAGCGCTTATGTTTGTTTGCCTTATTATTATGTGGCTTATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 GATGACCGGCTCAACCATCGCGCCCACAACGGACTATCGCAACACCACTGCTACCGGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGCCTAAAGCGCAGACGCGCCAGACCCCCCATCTATAGGCCTATCATTGTGCTCAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binant adenovirus comprising the polynucleotid
The recombinant adenovirus is designated Ads-
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4.1e-94;
                                                                                                                                                                                                                                           Barton K, Paielli D;
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100.0%; Pred. No. 4.1
:ive 0; Mismatches
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                                                                                                                                                                                                            (FORD-) FORD HEALTH SYSTEM HENRY
                                                                                                                                              09-JUL-2004; 2004WO-US022320.
                                                                                                                                                                              09-JUL-2003; 2003US-0486219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of a recombinant adenovirus
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                            Human adenovirus type
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                                                                                                             27-JAN-2005
                                               Synthetic
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Search completed: January 20, 2006, 19:29:31

chemotherapy, cytosine deaminase; SR39; herpes simplex virus type 1; thymidine kinase; death protein gene; cancer; neoplasm; 5-fluorocytosine;

Partial DNA sequence of AdS-yCD/mutTK(SR39)rep-ADP virus (E3 region).

(first entry)

07-APR-2005

ADW28317;

BP

ADW28317 standard; DNA; 917

RESULT 15 ADW28317

180

601

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Job time : 477 secs

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Sequence:

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Database

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AJ01917 Adenovirus
AJ293913 Human ade
AL651085 Sequence
TIG037 Adenovirus
AX259988 Sequence
AX26362 Sequence
AX26362 Sequence
AX26362 Sequence
AX084504 Sequence
AX084507 Sequence
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Henderson, D.R., Schuur, E.R. and Yu, D.-C.
Adenovirus vectors specific for cells expressing androgen receptor and methods of use thereof
Patent: US 6197293-A 21 06-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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100.0%; Score 307; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0; Indels
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Sequence 21 from patent US 6197293.
AR137114
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/mol_type="unassigned DNA"
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AX770200
ADRCG
HAD293913
HAD293915
AR651085
ADV16037
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AY339865
AR091533
AR102226
                                                           AX259957
AX259988
AX262362
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AR628961
AX084504
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AX084516
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Unclassified.
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AR137114
LOCUS
DEFINITION
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KEYWORDS
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BD070679 Adenoviru
BD195588 Adenoviru
BD117928 Adenoviru
BD217928 Adenoviru
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AR451690 Sequence
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AR452391 Human ade
AZ53991 Human ade
AZ53991 Human ade
AZ53991 Human ade
AZ53991 Human ade
                                                                   ; Search time 2114 Seconds (without alignments) 8254.938 Million cell updates/sec
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                                                                                                                                  1 gatgaccggctcaaccatcg......ttcttttacagtatgattaa 307
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         GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                   5883141 segs, 28421725653 residues
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5 AR160082
8 BD070679
8 BD195538
8 BD195538
8 BD217928
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AR223335
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AR451740
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Maximum Match 100%
Listing first 45 summaries
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                                                                      January 20, 2006, 18:56:50
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Maximum DB seq length: 200000000
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PAT 16-JUN-2001

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and methods of use thereof

Patent: JP 2001515351-A 21 18-SEP-2001;

CALYDON INC

OS Unidentified

PN JP 2001515351-A/21

PP 03-MAR-1998 JP 1998538696

PR 03-MAR-1999 JP 1998538696

PR 03-MAR-1997 US 60/039762,02-MAR-1998 US 09/033333 PI

DE CHAO YU,DANIEL R HENDERSON, ERIC R SCHUUR, HENRY G LAMPARSKI PC

CLON15/86,C12N5/10,A61K48/00,A61K47/48,C12Q1/70,C12N11/08 CC

Strandedness: Single;

CC Topology: Linear;

CC Adenovirus vectors specific for cells expressing androgen CC

receptor and

CC methods of use thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adenovirus vectors containing heterologous transcription regulatory elements and methods of using same.
BD195488
BD195488.1 GI:33005258
UP 2002514074-A/9.
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Henderson, D.R., Yu, D.C. and Lamparski, H.G.
Adenovirus vectors containing heterologous transcription regulatory
elements and methods of using same
Patent: JP 2002514074-A 9 14-MAY-2002;
CALYDON INC
OS Unidentified
PN JP 20021
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100.0%; Score 307; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0; Indels (
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/organism='Unidentified'
Location/Qualifiers
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Little, A.S., Henderson, D.R., Schuur, E.R. and Lamparski, H.
Ladenovirus vectors specific for cells expressing alpha-fetoprotein
and methods of use thereof
Patent: US 6254862-A 22 03-JUL-2001;
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Yu,D.C., Henderson,D.R., Schuur,E.R. and Lamparski,H.G.
Adenovirus vectors specific for cells expressing androgen receptor
      61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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BD070679
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/organism="unknown"
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JP 2001515351-A/21.
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Matches 307; Conservative
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Little, A.S., Lamparski, H.G., Henderson, D.R. and Schuur, E.R.
Adenovirus vector specific to cell expressing alpha-fetoprotein and
method of using the same
AL P2002516568-A 22 04-JUN-2002;
CALYDON INC
OS Artificial Sequence
PN JP 2002516568-A/22
PD 04-JUN-2002
PR 03-MAR-1998 JP 1998538676
PR 03-MAR-1999 JP 1998538676
PR 03-MAR-1997 US 60/039597,02-MAR-1998 US 09/033428 PI
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Adenovirus vector specific to cell expressing alpha-fetoprotein and
method of using the same.
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CI2N15/86,CI2N5/10,A61K48/00,A61K47/48,CI2Q1/70,CI2N11/08
Strandedness: Double,
CT Topology: Linear;
CC Adenovirus vectors specific for cells expressing CC
carcinoembryonic antigens
CC and methods of use thereof
FH Key Location/Qualifiers
FT CDS 2.304.
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Pred. No. 1e-83;
0; Mismatches 0;
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1 (bases 1 to 307)
                                                                                                                                                                                           /organism="unidentified"
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Nucleotide Sequence for ADP
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JP 2002516568-A/22.
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Best Local Similarity 100.0%;
Matches 307; Conservative 0
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PF 03-MAR-1998 JP 1998538674
PR 03-MAR-1999 US 60/039762,03-MAR-1997 US 60/039763 PR 03-MAR-1997 US 60/039763 PR 04-AUG-1997 US 60/05523,02-MAR-1998 US 09/033556 PI DANIEL R HENDERSON, DE CHAO YU, HENRY G LAMPARSKI PC C12N15/86,C12N5/10,A61K48/00,A61K47/48,C12N11/08 CC Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
CC Adenovirus vectors containing heterologous transcription CC
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G LAMPARSKI, DANIEL R HENDERSON, ERIC R SCHUUR PC
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Adenovirus vectors containing cell status-specific response
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C12N15/09, A61K48/00, A61P35/00, C12N1/15, C12N1/19, C12N1/21, C12N5/
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Yu,D.C. and Henderson,D.R.
Adenovirus vectors containing cell status-specific response elements and methods of use thereof
Patent: JP 2002525063-A 8 13-AUG-2002;
CALYDON INC
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                                                                                          Length 307;
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10-SEP-1999 JP 2000570347
10-SEP-1998 US 60/099791,09-SEP-1999 US
CHAO YU,DANIEL R HENDERSON
             1. .307
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241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
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Henderson, D.R., Schuur, E.R. and Yu, D.-C.
Adenovirus vectors specific for cells expressing androgen receptor
and methods of use thereof
Patent: US 6436394-A 21.20-AUG-2002;
Cell Genesys, Inc.; Foster City, CA
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  DB 6; Length 307;
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Sequence 21 from patent US 6436394.
AR223335.1 GI:23331486
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/mol_type="genomic DNA"
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PAT 20-FEB-2004
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1 (bases 1 to 307)

1 (bases 1 to 307)

Thenderson, D.R. and Schuur, B.R.

Tissue specific adenoviral vectors

Patent: US 6676935-A 61 13-JAN-2004;

Cell Genesys, Inc.; South San Francisco,

Location/Qualifiers
   Patent: US 6676935-A 10 13-JAN-2004;
Cell Genesys, Inc.; South San Francisco,
Location/Qualifiers
                                                                                                                                          Query Match
100.0%; Score 307; DB 6;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0
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Little, A.S., Henderson, D.R., Schuur, E.R. and Lamparski, H.
Little, A.S., Henderson, D.R., Schuur, E.R. and Lamparski, H.
Adenovirus vectors specific for cells expressing alpha-fetoprotein
and methods of use thereof.
Patent: US 6585968-A 22 01-JUL-2003;
Cell Genesys, Inc.; Poster City, CA
Location/Qualifiers
AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120
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100.0%; Score 307; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0; Indels (
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Sequence 22 from patent US 6585968.
AR349303. GI:33750029
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Unclassified.
1 (bases 1 to 307)
Henderson, D. R. and Schuur, E.R.
Tissue specific adenoviral vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
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                             1 (bases 1 to 307)
Yu, D.-C., Zhang, H. and Henderson, D.R.
Human and mouse uroplakin II gene transcriptional regulatory
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100.0%; Score 307; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0; Indels
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Unclassified.
1 (bases 1 to 307)
Yu,D.C. and Henderson,D.R.
Adenovirus vectors containing cell statu
elements and methods of use thereof
Patent: US 6900049-A 7 31-MAY-2005;
Cell Genesys, Inc.; San Francisco, CA
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Patent: US 6852528-A 3 08-FEB-2005;
Cell Genesys, Inc.; San Francisco, CA
Location/Qualifiers
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Sequence 7 from patent US 6900049.
AR669908
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/wol_type="genomic DNA"
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Yu, D.-C., Li, Y., Little, A.S. and Henderson, D.R.
Cell-specific adenovirus vectors comprising an internal ribosome entry site
Patent: US 6692736-A 17 17-FEB-2004;
Cell Genesys, Inc.; South San Francisco, CA
Location/Qualifiers
1. 307
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AR474487
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Sequence 3 from patent US 6852528.
AR635125
AR635125.1 GI:59793252
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/mol_type="genomic DNA"
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Matches 307; Conservative
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0y 61 AACATCTGCCCTAAATTTACCCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120 0b 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCCTTTGTCAATGACTGGGCGAGCTTGGA 120 0y 121 CATGTGGTGGTTTTCCATAGGGCTTATTGTTTGCCTTATTATTATTATTGTGGCTTATTTG 180 121 CATGTGGTGGTTTTCCATAGGCTTATGTTTGCTTATTATTATTATTTTG 180 121 CATGTGGTGGTTTTCCATAGGCTTATGTTTGCTTATTATTATTATTTTG 180 0y 181 TTGCCTAAAGCGCAGAGGCGCCAGACCCCCATCTATAGGCCTATCATTGTGCTCAACCC 240 0y 241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCCATCTTTTTACAGTA 300 0y 241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTTTTTACAGTA 300 0y 301 TGATTAA 307 0b 301 TGATTAA 307 0b 301 TGATTAA 307	p e	် နေ့ရှိ ပိ	/organism="Human adenovirus type 2" /virion /wirion /wirion /mol type="qenomic DNA" /isoTate="R05" /isoTate="R05" / ppecific host="Homo sapiens" /db_xref="taxon:10515" /map="0.76-0.86" /tissue_type="respiratory epithelium" /country="Germany:Lower Saxony" /tissue_type="respiratory epithelium" /country="Germany:Lower Saxony" /1. :255 /gene="protein VIII" /codon start=1 /product="L4 protein VIII" /product="L4 protein VIII" /product="L4 protein VIII" /product="L4 protein VIII" /product="L4 protein VIII"	/translation="LileOpAlTTTPRNNLNPRSWPAALVYQESPAPTTVVLPRDAQA

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121	2211	181	2271	241	2331	301	2391	
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